

FIGURE 1



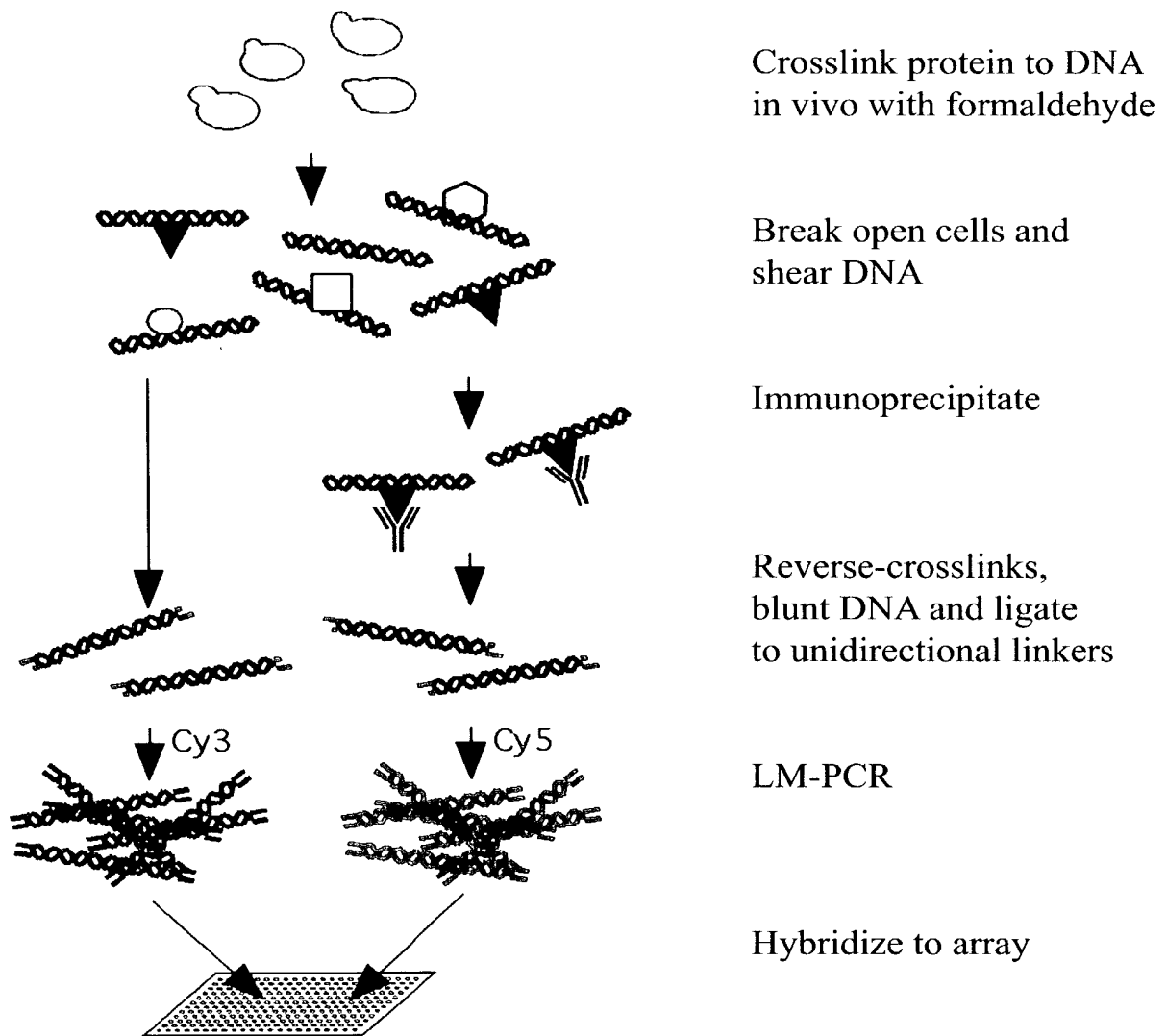


FIGURE 1



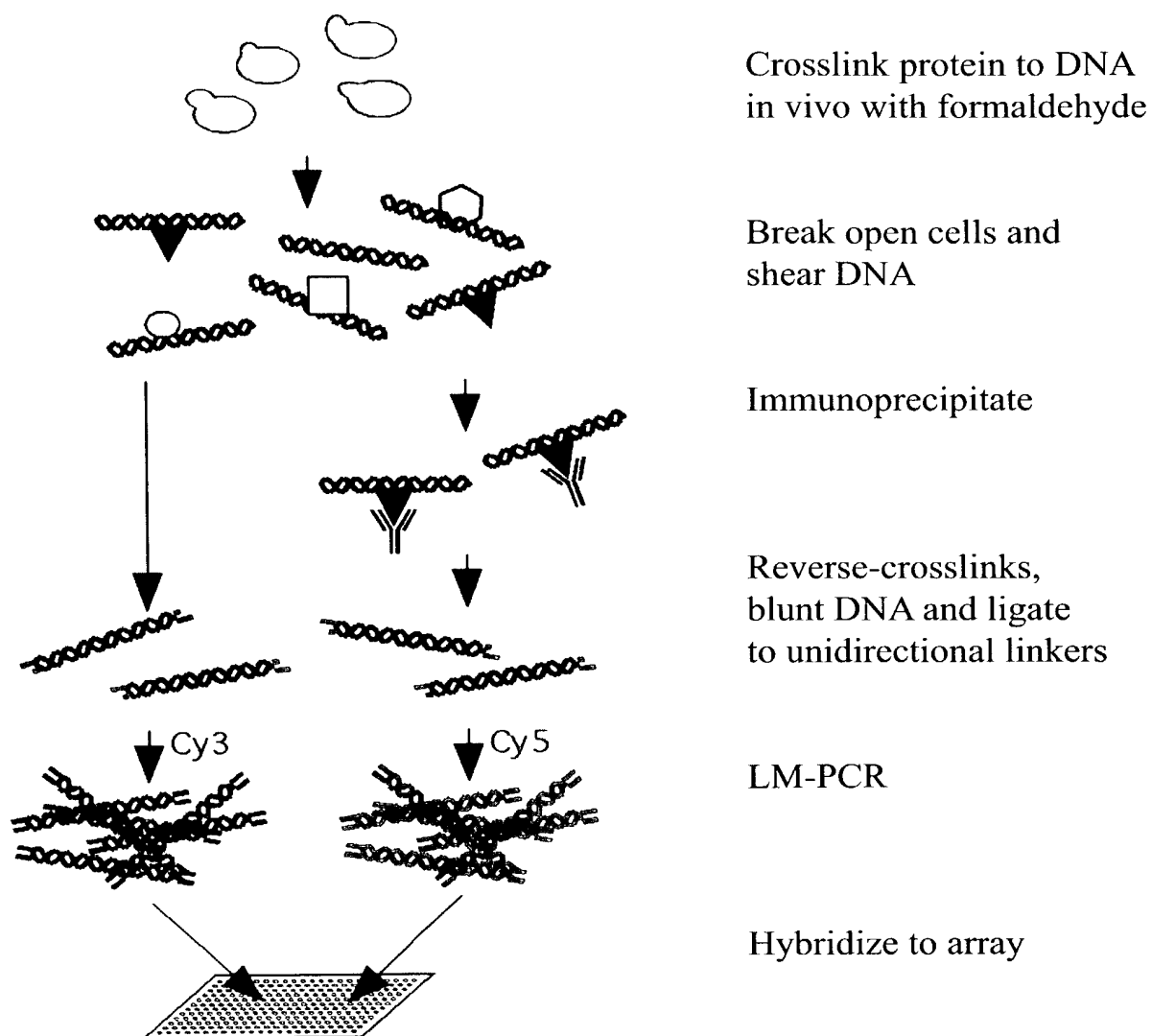


FIGURE 1



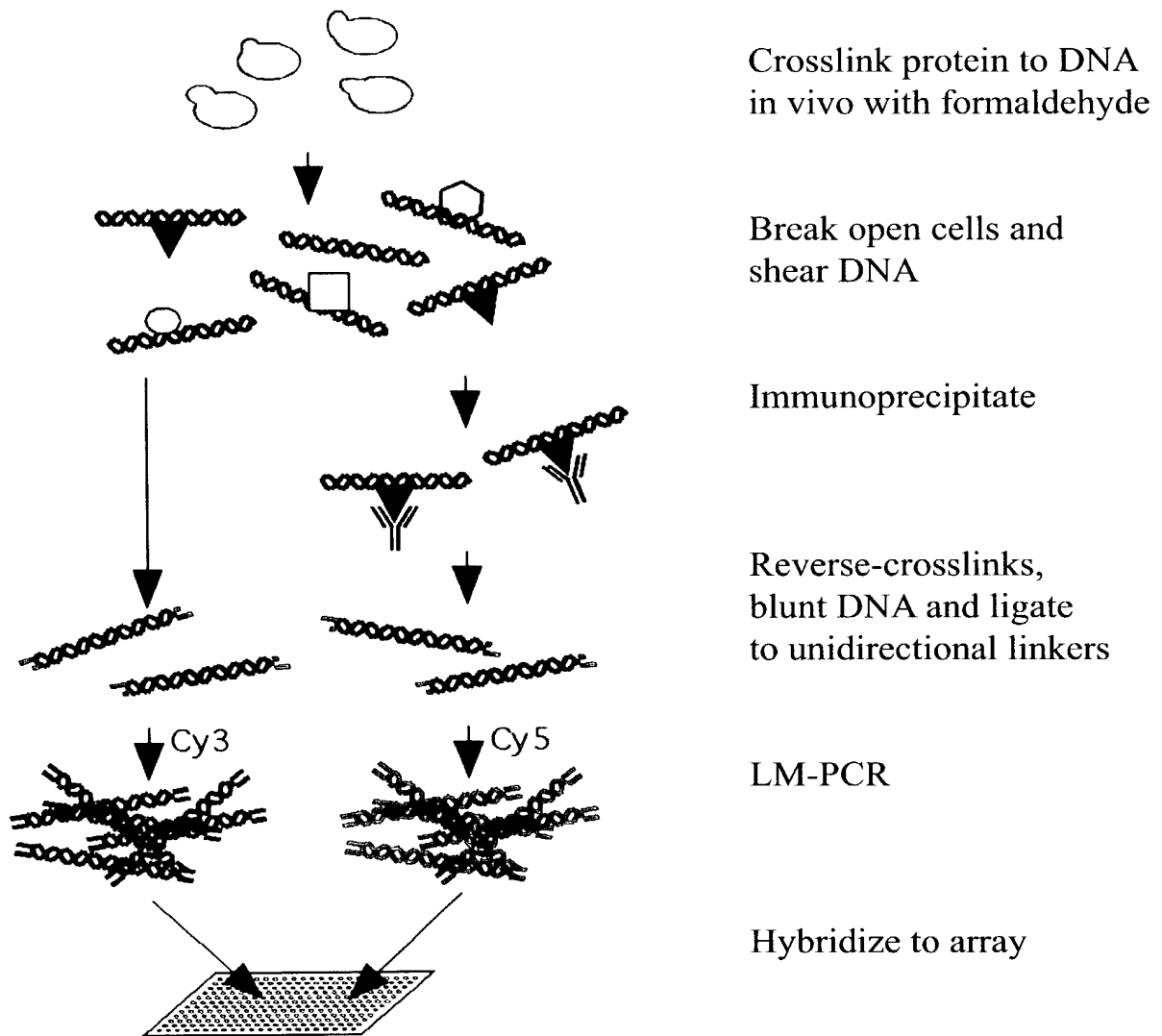


FIGURE 1



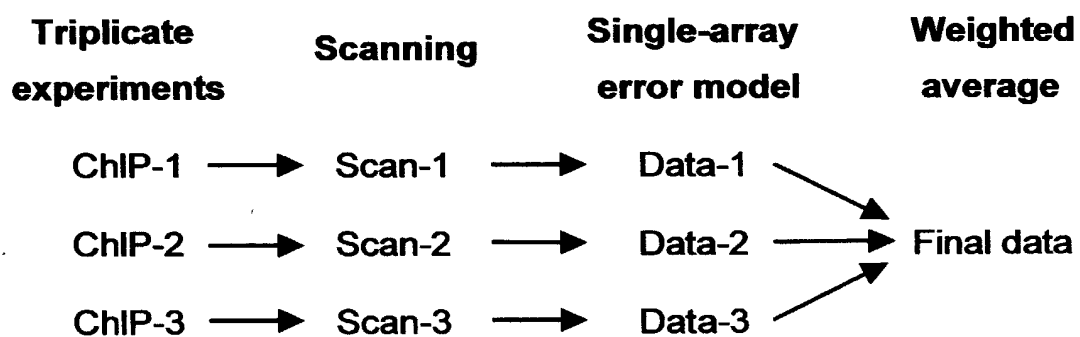
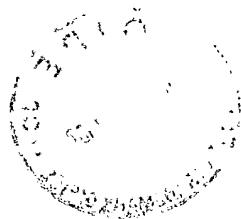


FIGURE 2



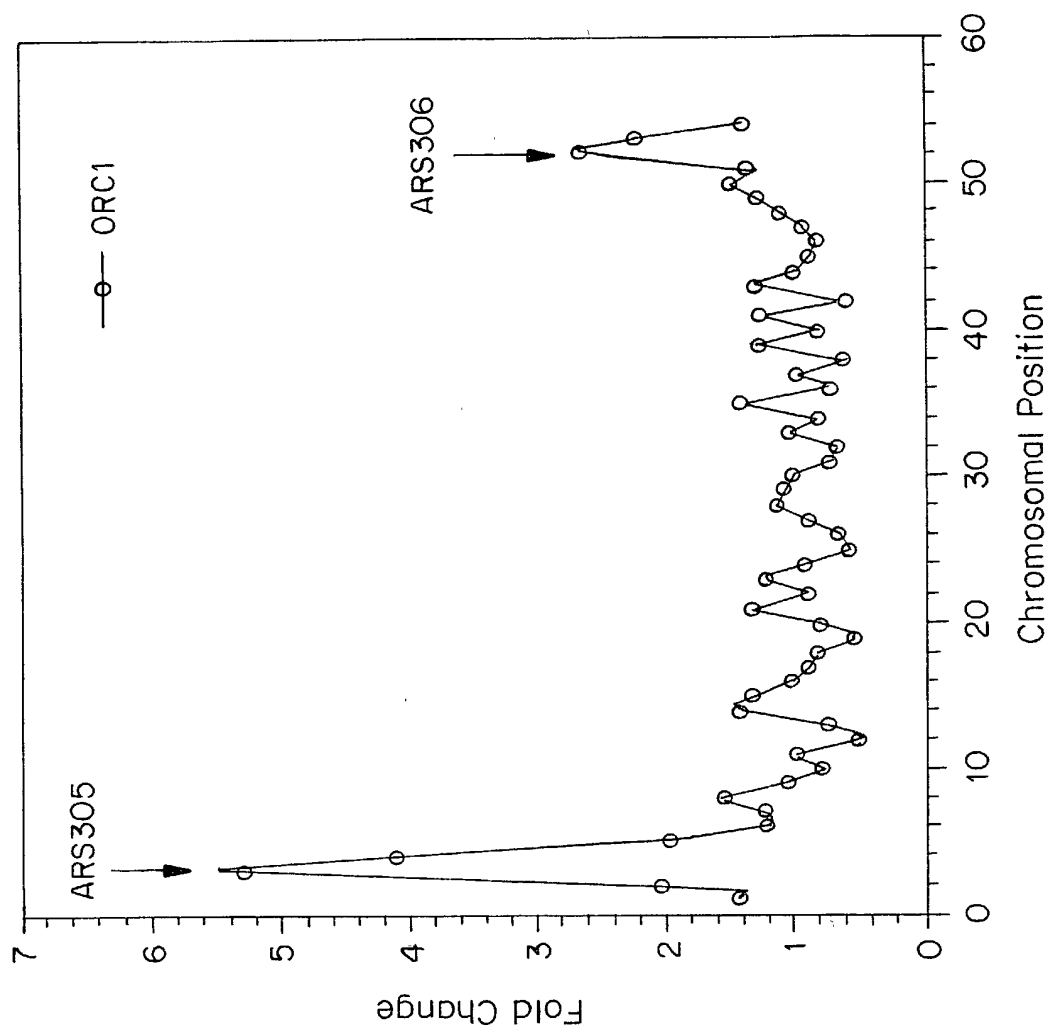


FIG. 3

Interests:
 RNA Polymerase II
 SRB/Mediator Complex
 General Transcription Factors
 SWI/SNF Complex
 SAGA
 ORC complex
 DNA Polymerase

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

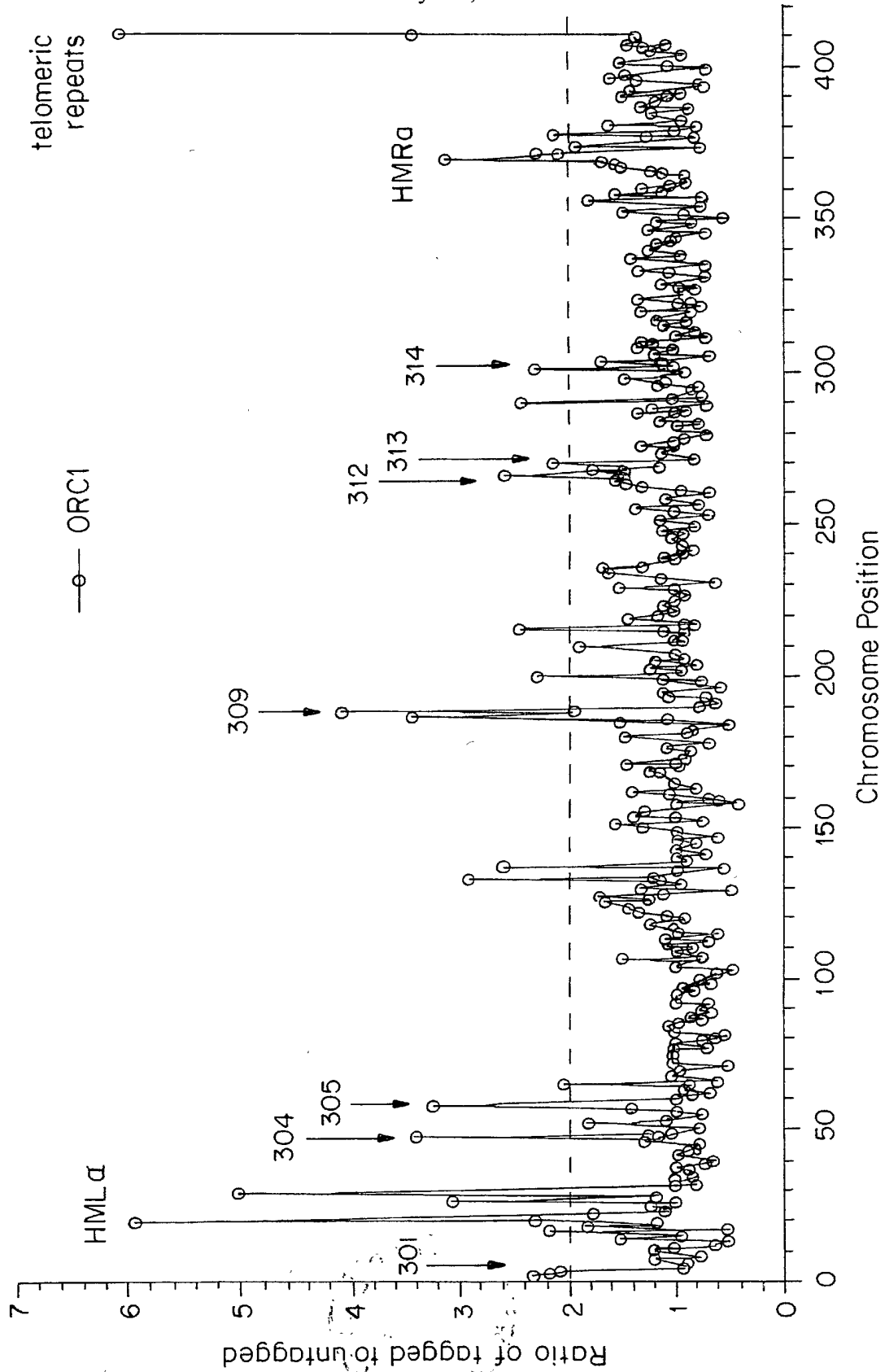


FIG. 4

App No.: 10/032,281

10/032,281, 06/06/12

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

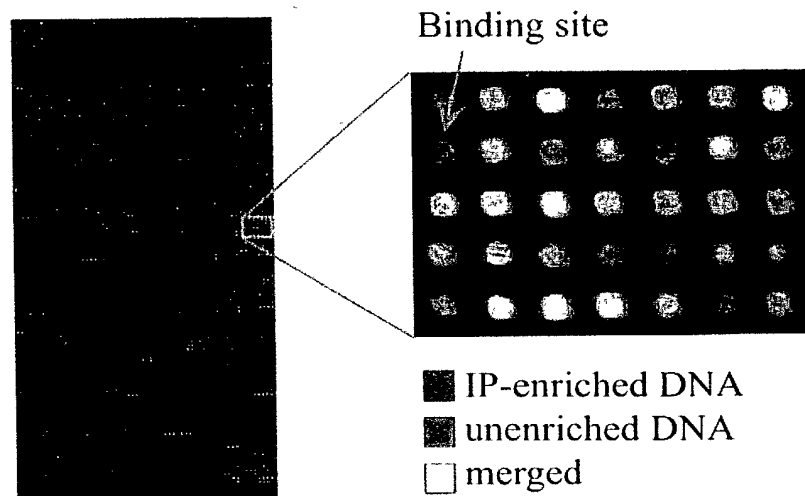


FIGURE 5A

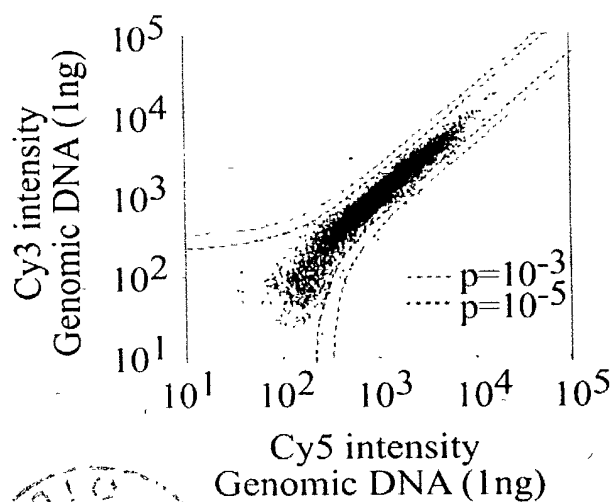


FIGURE 5B



App No.: 10/032,281

Pub. No. 2005/022931 A1

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

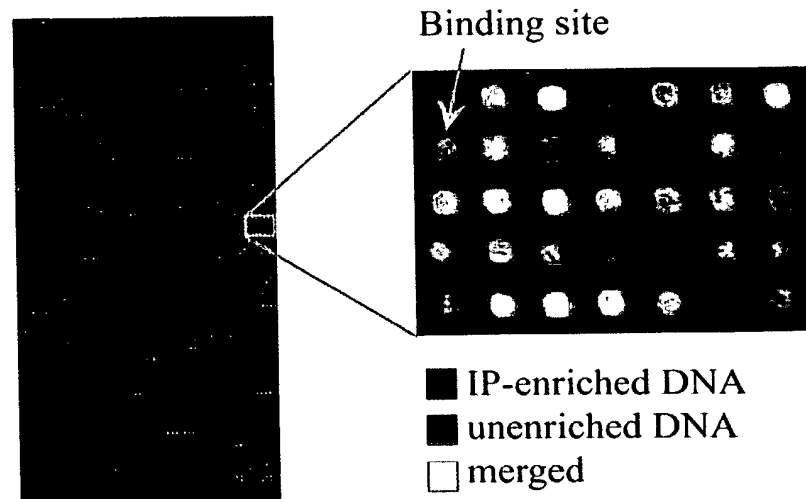


FIGURE 5A

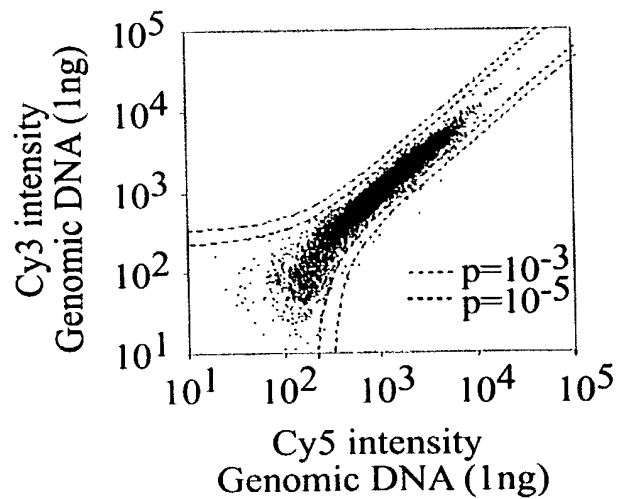


FIGURE 5B

App No.: 10/032,281

1002 FEB 1 06 06 PM

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

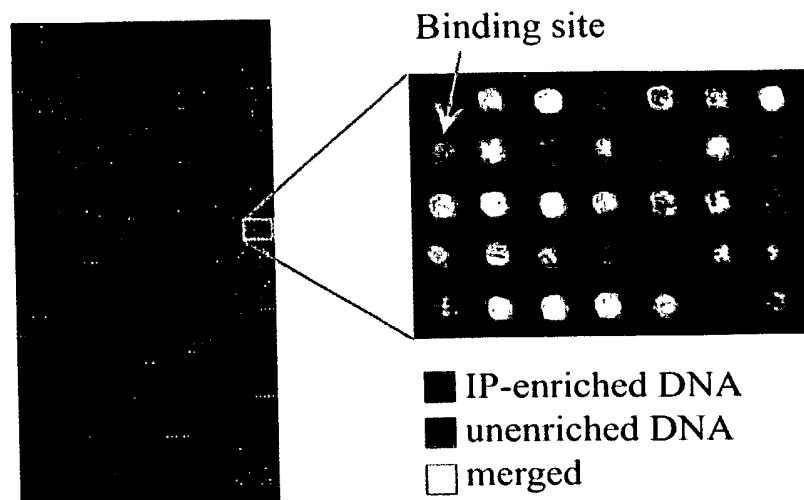


FIGURE 5A

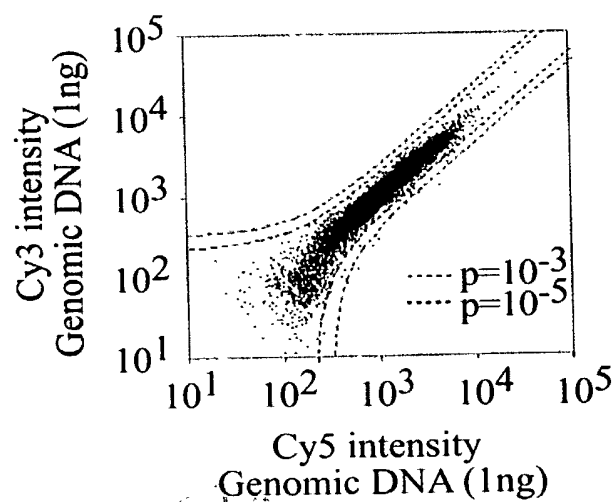


FIGURE 5B

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

10032281-060502

Glucose	Galactose	Expression (Gal/Glu)	Binding		Name	Binding		Expression	
			Ratio	p-value		Ratio	p-value	Ratio	Description
			2.8	2.5X10-02	GAL2	9.5	1.5X10-10	188.6	Galactose permease
			1.4	5.4X10-01	GAL3	8.2	3.5X10-10	18.2	Regulatory protein required for rapid induction of galactose pathway
			0.4	2.0X10+00	GAL7	8.2	6.4X10-10	170.1	UDP-glucose-hexose-1-phosphate uridylyltransferase
			1.3	6.0X10-01	GAL1	7.8	1.5X10-09	271.3	Galactokinase, first step in galactose metabolism
			1.3	6.0X10-01	GAL10	7.8	1.5X10-09	118.8	UDP-glucose 4-epimerase
			0.3	2.0X10+00	FUR4	4.6	4.3X10-08	4.6	Uracil permease (adjacent to GAL1)
			0.9	1.2X10+00	GXY1	4.3	1.3X10-07	93.1	Galactose-induced oxidoreductase
			0.9	1.2X10+00	MTH1	4.0	2.4X10-07	21.6	Repressor of hexose transport genes
			0.5	1.9X10+00	GAL80	3.7	7.0X10-07	4.0	Negative regulator for expression of galactose-induced genes
			0.6	1.8X10+00	PCL10	3.0	8.8X10-06	2.6	Cyclin that associates with Pho85p, involved in glycogen accumulation
			3.7	1.7X10-02	YBR022W	10.4	1.2X10-10	1.5	Unknown function (adjacent to GAL1)
			1.4	5.5X10-01	YDR008C	8.2	3.5X10-10	1.5	Unknown function (share intergenic region with GAL3)
			2.7	2.9X10-02	GIS3	8.0	4.8X10-10	1.0	Multicopy suppressor of the Gal(-) phenotype of snf1 mgl1 srb8/10/11 cells
			0.6	1.9X10+00	TLC1	4.2	1.2X10-07	1.0	RNA subunit of telomerase
			0.6	1.9X10+00	PDX3	4.2	1.2X10-07	1.6	Pyridoxine phosphate oxidase
			0.9	1.2X10+00	RI01	4.3	1.3X10-07	1.4	Unknown function (share intergenic region with GXY1)
			2.3	6.6X10-02	YJR044C	4.0	3.4X10-07	1.7	Unknown function
			0.9	1.1X10+00	SNQ2	3.5	1.1X10-06	0.6	Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)
			0.9	1.1X10+00	YDR010C	3.5	1.1X10-06	1.0	Unknown function (adjacent to GAL3)
			1.9	1.9X10-01	APC9	3.8	2.0X10-06	1.2	Component of the anaphase-promoting complex (APC)
			0.5	1.9X10+00	CSG2	3.3	2.4X10-06	1.3	Required for synthesis of the mannosylated sphingolipids
			0.9	1.3X10+00	RPL4B	3.3	2.8X10-06	0.8	Ribosomal protein L4, Gene (adjacent to GAL3)
			0.6	1.8X10+00	YGL132W	3.0	9.1X10-06	1.0	Unknown function, (adjacent to PCL10)
			1.5	4.1X10-01	CHA4	3.1	9.8X10-06	1.0	Zinc-finger protein required for transcriptional activation of CHA1

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

Binding		Expression		Binding		Expression	
Glucose	Galactose	Ratio	p-value	Glucose	Galactose	Ratio	p-value
Name	Ratio	p-value	Description	Name	Ratio	p-value	Description
GAL2	2.8	2.5X10-02	9.5	1.5X10-10	188.6	Galactose permease	
GAL3	1.4	5.4X10-01	8.2	3.5X10-10	18.2	Regulatory protein required for rapid induction of galactose pathway	
GAL7	0.4	2.0X10+00	8.2	6.4X10-10	170.1	UDP-glucose-hexose-1-phosphate uridylyltransferase	
GAL1	1.3	6.0X10-01	7.8	1.5X10-09	271.3	Galactokinase, first step in galactose metabolism	
GAL10	1.3	6.0X10-01	7.8	1.5X10-09	118.8	UDP-glucose 4-epimerase	
FUR4	0.3	2.0X10+00	4.6	4.3X10-08	4.6	Uracil permease (adjacent to GAL1)	
GCV1	0.9	1.2X10+00	4.3	1.3X10-07	93.1	Galactose-induced oxidoreductase	
MTH1	0.9	1.2X10+00	4.0	2.4X10-07	21.6	Repressor of hexose transport genes	
GAL80	0.5	1.9X10+00	3.7	7.0X10-07	4.0	Negative regulator for expression of galactose-induced genes	
PCL10	0.6	1.8X10+00	3.0	8.8X10-06	2.6	Cyclin that associates with Pho85p, involved in glycogen accumulation	
YBR022W	3.7	1.7X10-02	10.4	1.2X10-10	1.5	Unknown function (adjacent to GAL1)	
YDR008C	1.4	5.5X10-01	8.2	3.5X10-10	1.5	Unknown function (share intergenic region with GAL3)	
GIS3	2.7	2.9X10-02	8.0	4.8X10-10	1.0	Multicopy suppressor of the Gal(-) phenotype of snf1 mig1 srb8/10/11 cells	
TLC1	0.6	1.9X10+00	4.2	1.2X10-07	1.0	RNA subunit of telomerase	
PDX3	0.6	1.9X10+00	4.2	1.2X10-07	1.6	Pyridoxine phosphate oxidase	
RIO1	0.9	1.2X10+00	4.3	1.3X10-07	1.4	Unknown function (share intergenic region with GCV1)	
YJR044C	2.3	6.6X10-02	4.0	3.4X10-07	1.7	Unknown function	
SNQ2	0.9	1.1X10+00	3.5	1.1X10-06	0.6	Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)	
YDR010C	0.9	1.1X10+00	3.5	1.1X10-06	1.0	Unknown function (adjacent to GAL3)	
APC9	1.9	1.9X10-01	3.8	2.0X10-06	1.2	Component of the anaphase-promoting complex (APC)	
CSG2	0.5	1.9X10+00	3.3	2.4X10-06	1.3	Required for synthesis of the mannosylated sphingolipids	
RPL4B	0.9	1.3X10+00	3.3	2.8X10-06	0.8	Ribosomal protein L4, Gene (adjacent to GAL3)	
YGL132W	0.6	1.8X10+00	3.0	9.1X10-06	1.0	Unknown function, (adjacent to PCL10)	
CHA4	1.5	4.1X10-01	3.1	9.8X10-06	1.0	Zinc-finger protein required for transcriptional activation of CHA1	

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

Glucose	Galactose	Expression (Gal/Glu)	Name	Binding		Expression	
				Glucose Ratio p-value	Galactose Ratio p-value	Ratio Gal/Glu	Description
			GAL2	2.8 2.5X10-02	9.5 1.5X10-10	188.6	Galactose permease
			GAL3	1.4 5.4X10-01	8.2 3.5X10-10	18.2	Regulatory protein required for rapid induction of galactose pathway
			GAL7	0.4 2.0X10+00	8.2 6.4X10-10	170.1	UDP-glucose-hexose-1-phosphate uridylyltransferase
			GAL1	1.3 6.0X10-01	7.8 1.5X10-09	271.3	Galactokinase, first step in galactose metabolism
			GAL10	1.3 6.0X10-01	7.8 1.5X10-09	118.8	UDP-glucose 4-epimerase
			FUR4	0.3 2.0X10+00	4.6 4.3X10-08	4.6	Uracil permease (adjacent to GAL1)
			GCY1	0.9 1.2X10+00	4.3 1.3X10-07	93.1	Galactose-induced oxidoreductase
			MTH1	0.9 1.2X10+00	4.0 2.4X10-07	21.6	Repressor of hexose transport genes
			GAL80	0.5 1.9X10+00	3.7 7.0X10-07	4.0	Negative regulator for expression of galactose-induced genes
			PCL10	0.6 1.8X10+00	3.0 8.8X10-06	2.6	Cyclin that associates with Pho85p, involved in glycogen accumulation
			YBR022W	3.7 1.7X10-02	10.4 1.2X10-10	1.5	Unknown function (adjacent to GAL1)
			YDR008C	1.4 5.5X10-01	8.2 3.5X10-10	1.5	Unknown function (share intergenic region with GAL3)
			GIS3	2.7 2.9X10-02	8.0 4.8X10-10	1.0	Multicopy suppressor of the Gal(-) phenotype of snf1 mig1 srb8/10/11 cells
			TLC1	0.6 1.9X10+00	4.2 1.2X10-07	1.0	RNA subunit of telomerase
			PDX3	0.6 1.9X10+00	4.2 1.2X10-07	1.6	Pyridoxine phosphate oxidase
			RIO1	0.9 1.2X10+00	4.3 1.3X10-07	1.4	Unknown function (share intergenic region with GCY1)
			YJR044C	2.3 6.6X10-02	4.0 3.4X10-07	1.7	Unknown function
			SNQ2	0.9 1.1X10+00	3.5 1.1X10-06	0.6	Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)
			YDR010C	0.9 1.1X10+00	3.5 1.1X10-06	1.0	Unknown function (adjacent to GAL3)
			APC9	1.9 1.9X10-01	3.8 2.0X10-06	1.2	Component of the anaphase-promoting complex (APC)
			CSG2	0.5 1.9X10+00	3.3 2.4X10-06	1.3	Required for synthesis of the mannosylated sphingolipids
			RPL4B	0.9 1.3X10+00	3.3 2.8X10-06	0.8	Ribosomal protein L4, Gene (adjacent to GAL3)
			YGL132W	0.6 1.8X10+00	3.0 9.1X10-06	1.0	Unknown function, (adjacent to PCL10)
			CHA4	1.5 4.1X10-01	3.1 9.8X10-06	1.0	Zinc-finger protein required for transcriptional activation of CHA1

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

10032281, 060502

Glucose	Galactose	Expression	Name	Binding		Ratio	Gal/Glu	Description
				Glucose	Galactose			
Ratio	p-value			Ratio	p-value			
2.8	2.5X10 ⁻⁰²	9.5	1.5X10 ⁻¹⁰	188.6	Galactose permease			
1.4	5.4X10 ⁻⁰¹	8.2	3.5X10 ⁻¹⁰	18.2	Regulatory protein required for rapid induction of galactose pathway			
0.4	2.0X10 ⁺⁰⁰	8.2	6.4X10 ⁻¹⁰	170.1	UDP-glucose-hexose-1-phosphate uridylyltransferase			
1.3	6.0X10 ⁻⁰¹	7.8	1.5X10 ⁻⁰⁹	271.3	Galactokinase, first step in galactose metabolism			
1.3	6.0X10 ⁻⁰¹	7.8	1.5X10 ⁻⁰⁹	118.8	UDP-glucose 4-epimerase			
0.3	2.0X10 ⁺⁰⁰	4.6	4.3X10 ⁻⁰⁸	4.6	Uracil permease (adjacent to GAL1)			
0.9	1.2X10 ⁺⁰⁰	4.3	1.3X10 ⁻⁰⁷	93.1	Galactose-induced oxidoreductase			
0.9	1.2X10 ⁺⁰⁰	4.0	2.4X10 ⁻⁰⁷	21.6	Repressor of hexose transport genes			
0.5	1.9X10 ⁺⁰⁰	3.7	7.0X10 ⁻⁰⁷	4.0	Negative regulator for expression of galactose-induced genes			
0.6	1.8X10 ⁺⁰⁰	3.0	8.8X10 ⁻⁰⁶	2.6	Cyclin that associates with Pho85p, involved in glycogen accumulation			
YBR022W	3.7	1.7X10 ⁻⁰²	10.4	1.2X10 ⁻¹⁰	1.5	Unknown function (adjacent to GAL1)		
YDR008C	1.4	5.5X10 ⁻⁰¹	8.2	3.5X10 ⁻¹⁰	1.5	Unknown function (share intergenic region with GAL3)		
GIS3	2.7	2.9X10 ⁻⁰²	8.0	4.8X10 ⁻¹⁰	1.0	Multicopy suppressor of the Gal(-) phenotype of snf1 mig1 srb8/10/11 cells		
TLC1	0.6	1.9X10 ⁺⁰⁰	4.2	1.2X10 ⁻⁰⁷	1.0	RNA subunit of telomerase		
PDX3	0.6	1.9X10 ⁺⁰⁰	4.2	1.2X10 ⁻⁰⁷	1.6	Pyridoxine phosphate oxidase		
RIO1	0.9	1.2X10 ⁺⁰⁰	4.3	1.3X10 ⁻⁰⁷	1.4	Unknown function (share intergenic region with GCY1)		
YJR044C	2.3	6.6X10 ⁻⁰²	4.0	3.4X10 ⁻⁰⁷	1.7	Unknown function		
SNQ2	0.9	1.1X10 ⁺⁰⁰	3.5	1.1X10 ⁻⁰⁶	0.6	Drug-efflux pump involved in resistance to multiple drugs (adjacent to GAL3)		
YDR010C	0.9	1.1X10 ⁺⁰⁰	3.5	1.1X10 ⁻⁰⁶	1.0	Unknown function (adjacent to GAL3)		
APC9	1.9	1.9X10 ⁻⁰¹	3.8	2.0X10 ⁻⁰⁶	1.2	Component of the anaphase-promoting complex (APC)		
CSG2	0.5	1.9X10 ⁺⁰⁰	3.3	2.4X10 ⁻⁰⁶	1.3	Required for synthesis of the mannosylated sphingolipids		
RPL4B	0.9	1.3X10 ⁺⁰⁰	3.3	2.8X10 ⁻⁰⁶	0.8	Ribosomal protein L4, Gene (adjacent to GAL3)		
YGL132W	0.6	1.8X10 ⁺⁰⁰	3.0	9.1X10 ⁻⁰⁶	1.0	Unknown function, (adjacent to PCL10)		
CHA4	1.5	4.1X10 ⁻⁰¹	3.1	9.8X10 ⁻⁰⁶	1.0	Zinc-finger protein required for transcriptional activation of CHA1		

<1:1 >3/1 >5/1 <1/5 1/1 >5/1

FIGURE 6A

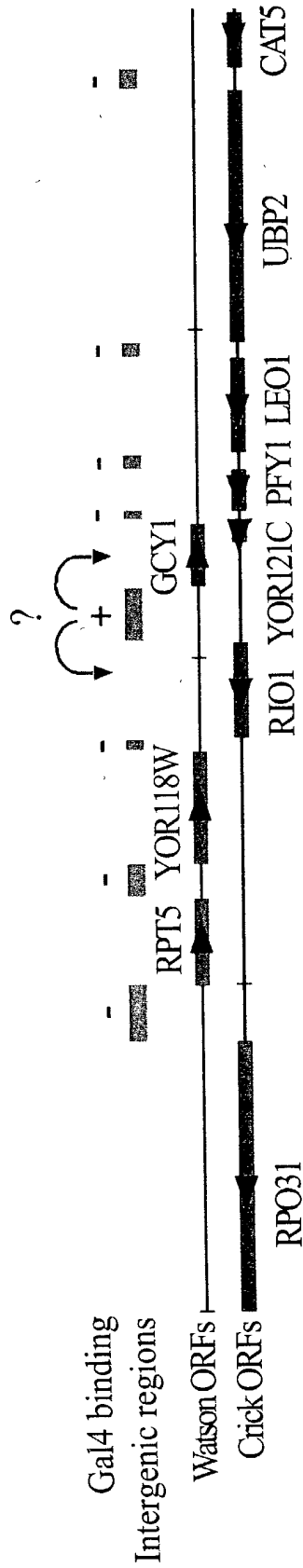


FIGURE 6B

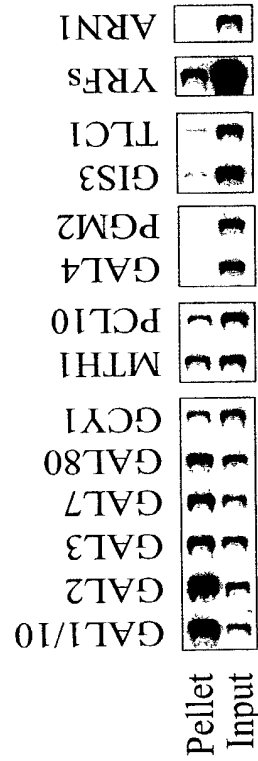


FIGURE 6C

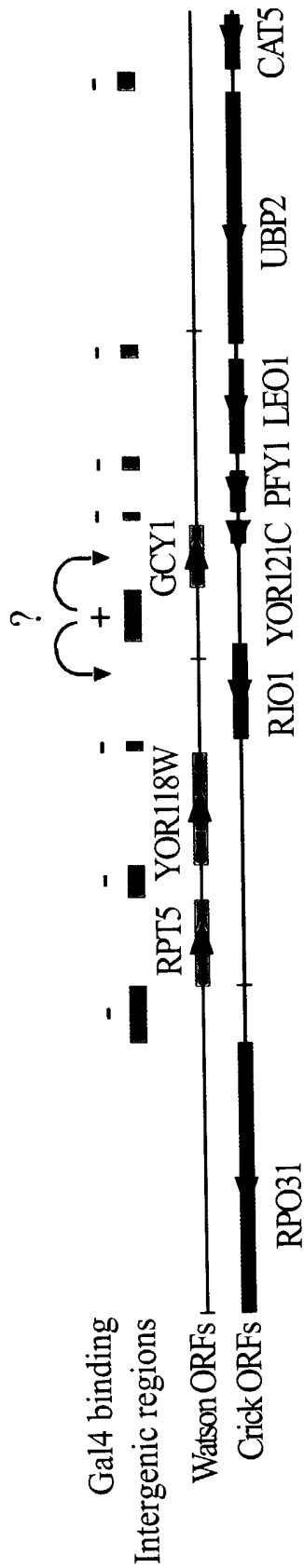


FIGURE 6B

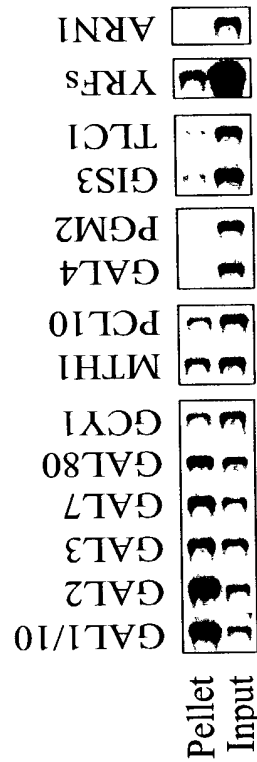


FIGURE 6C

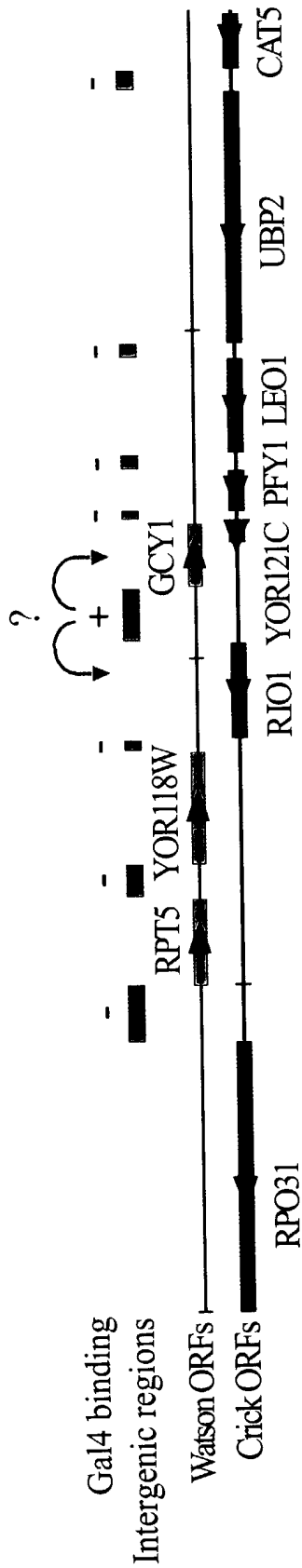


FIGURE 6B

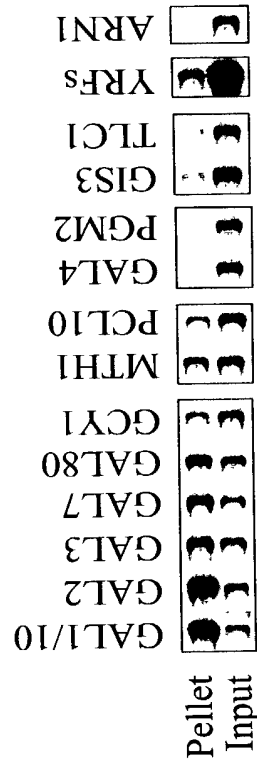


FIGURE 6C

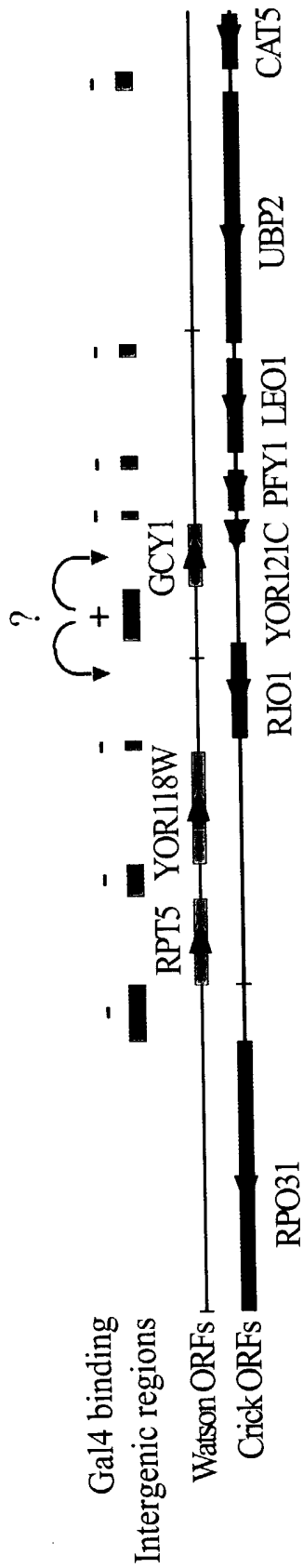


FIGURE 6B

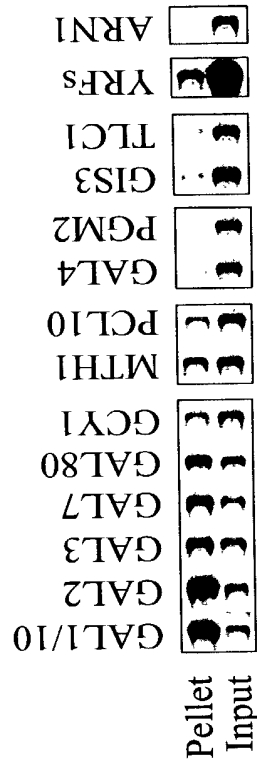


FIGURE 6C

App No.: 10/032,281

10052231, 050502

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

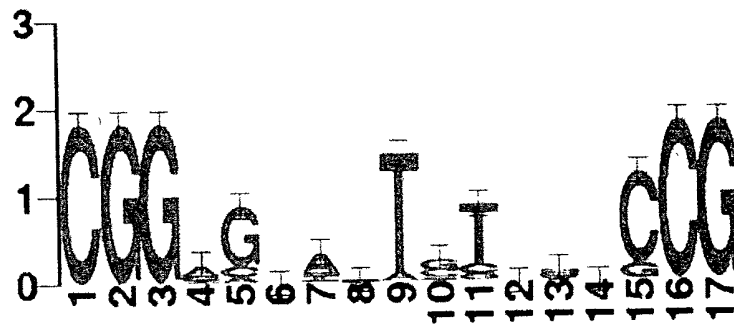


FIGURE 6D



App No.: 10/032,281

U.S. Pat. No. 7,545,019

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

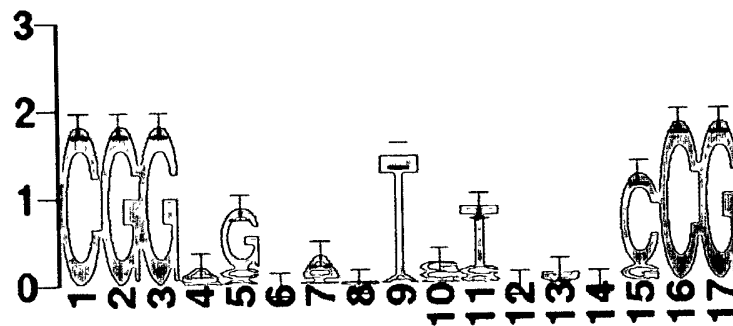
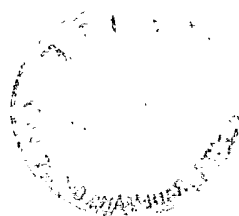


FIGURE 6D



App No.: 10/032,281

10/032,281, 05/15/12

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

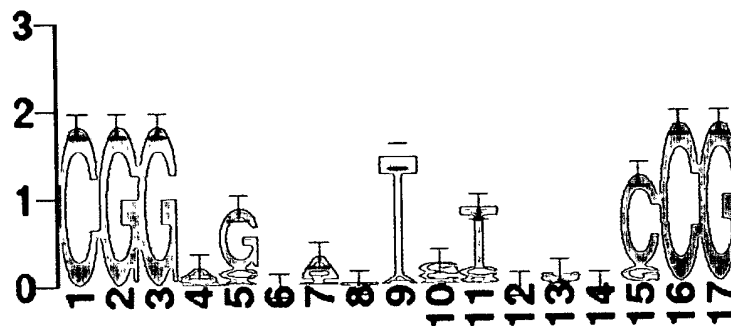
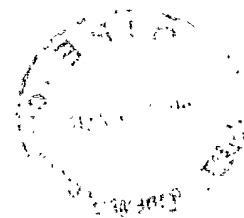


FIGURE 6D



App No.: 10/032,281
Title: Genome-Wide Location and Function...
Inventors: John Wyrick, *et al.*

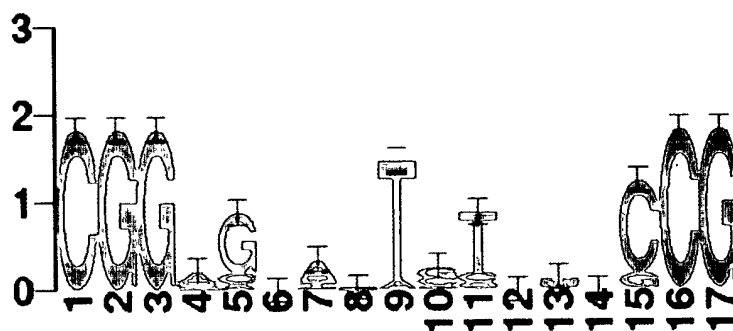


FIGURE 6D



App No.: 10/032,281

10/032,281, 06/05/02

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

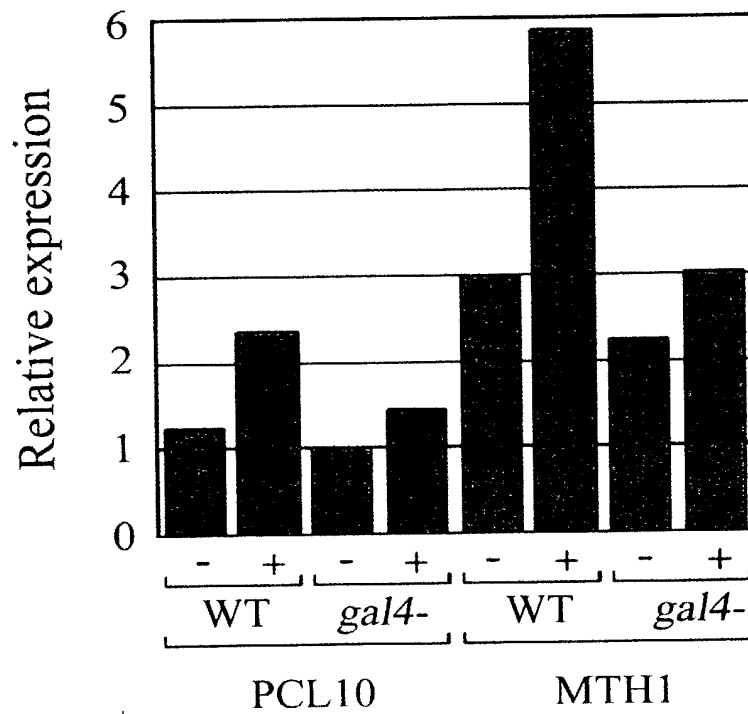


FIGURE 6E



App No.: 10/032,281

7/10/2006 10:00:00 AM

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

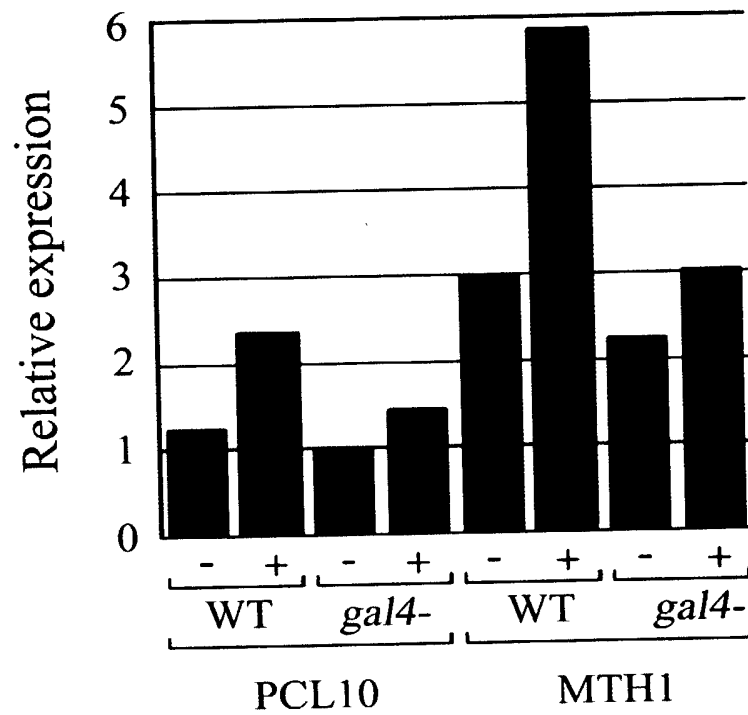
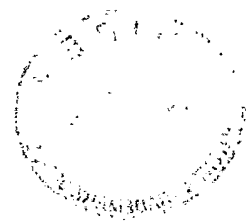


FIGURE 6E



App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

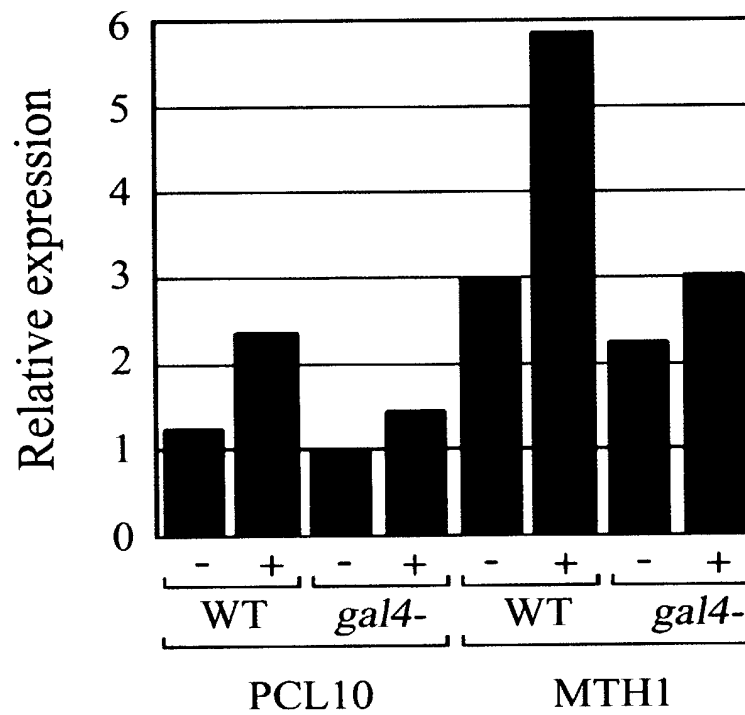


FIGURE 6E



App No.: 10/032,281

10/032,281 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

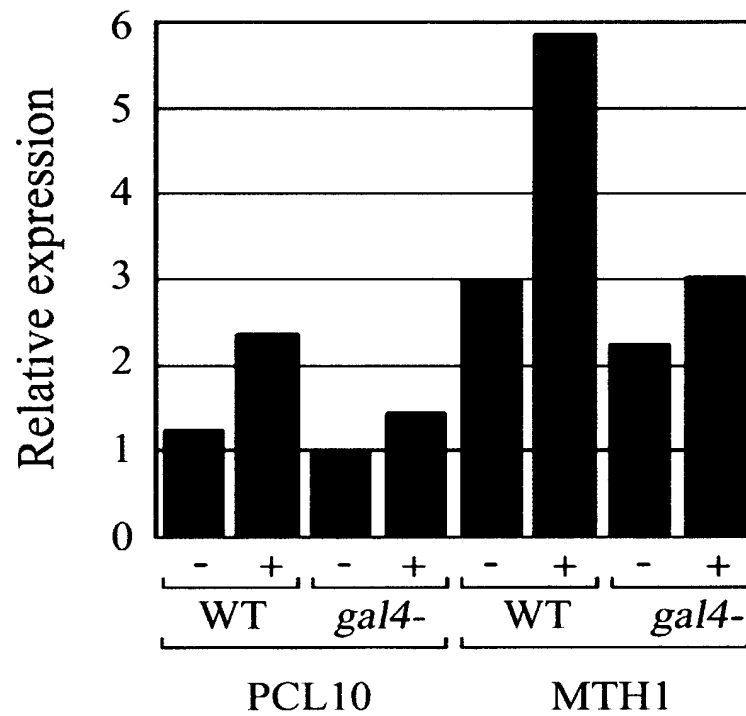
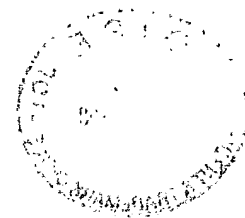


FIGURE 6E



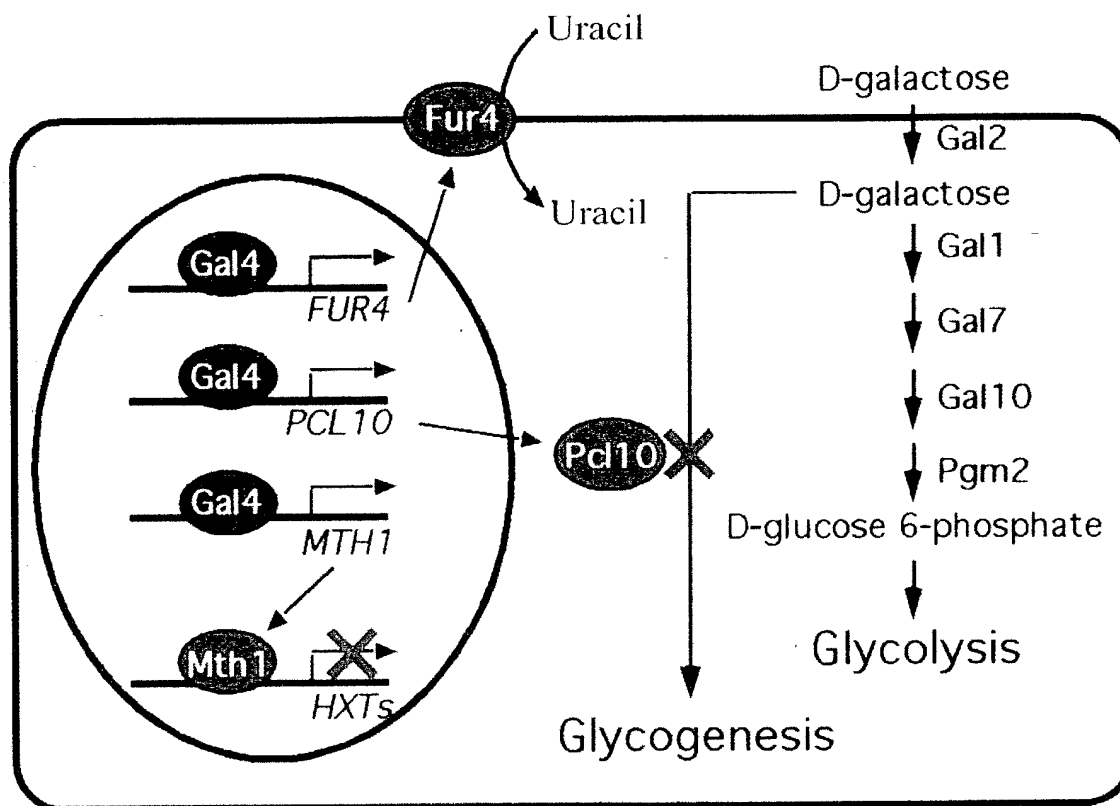


FIGURE 6F



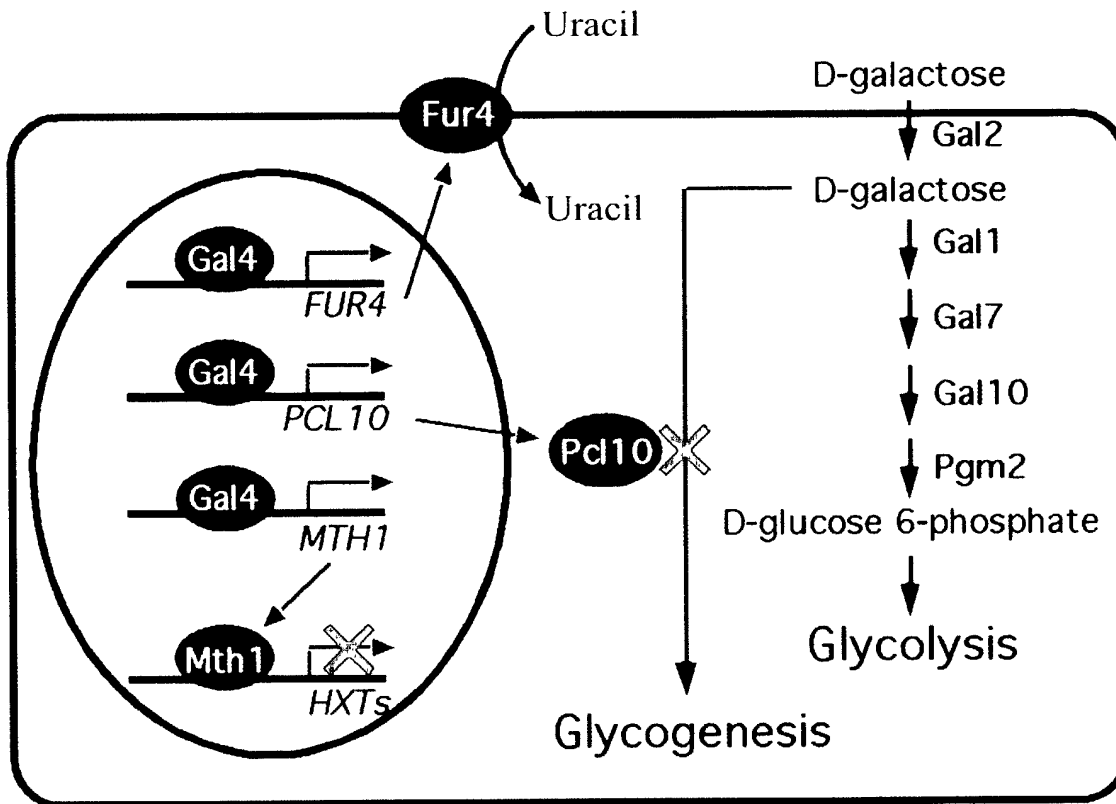


FIGURE 6F



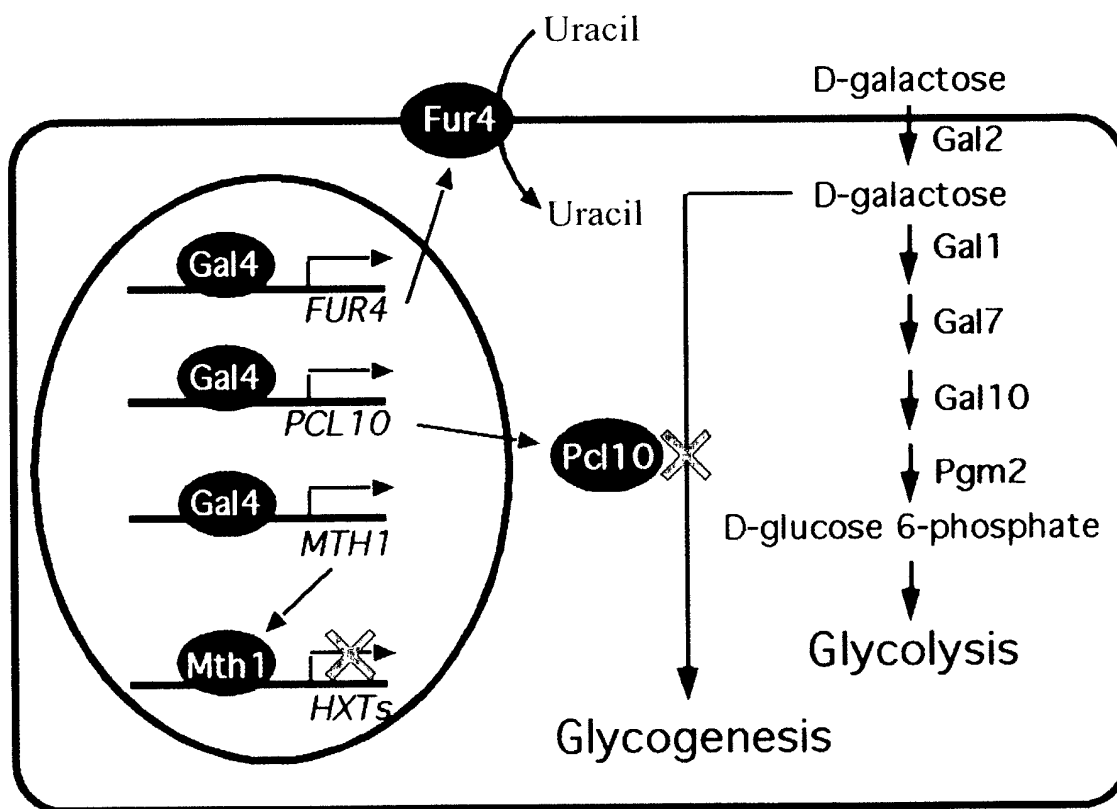
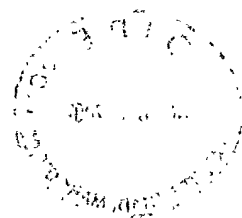


FIGURE 6F



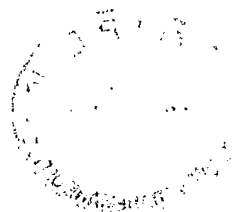


FIGURE 6F

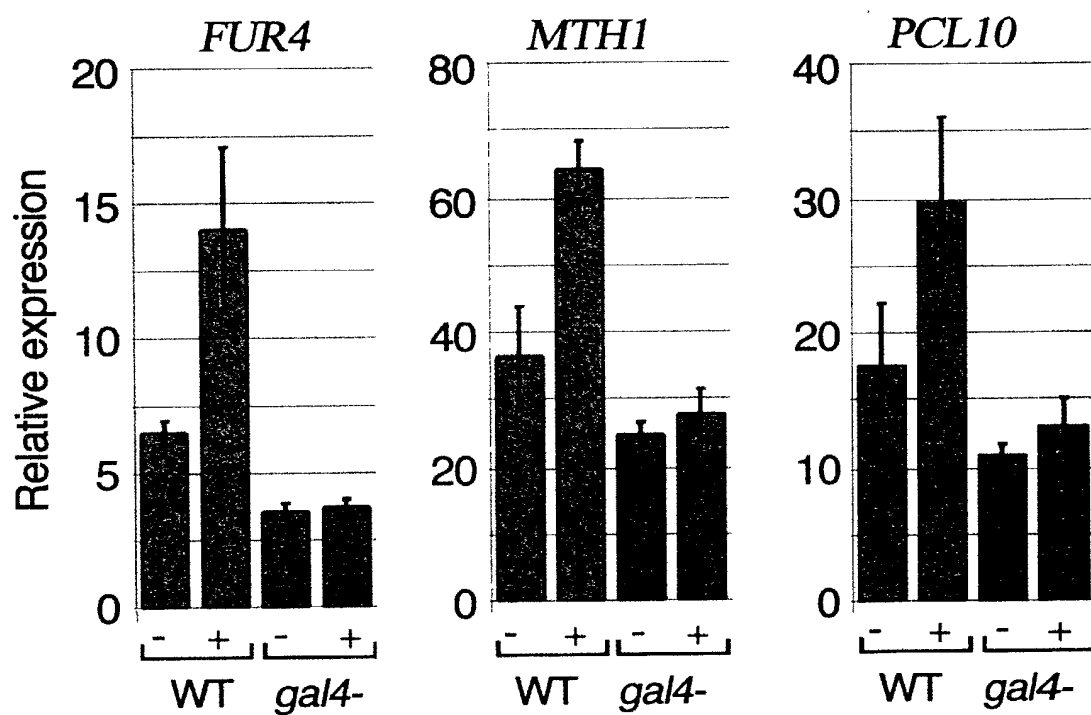
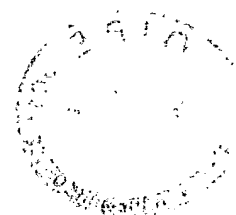


FIGURE 6G



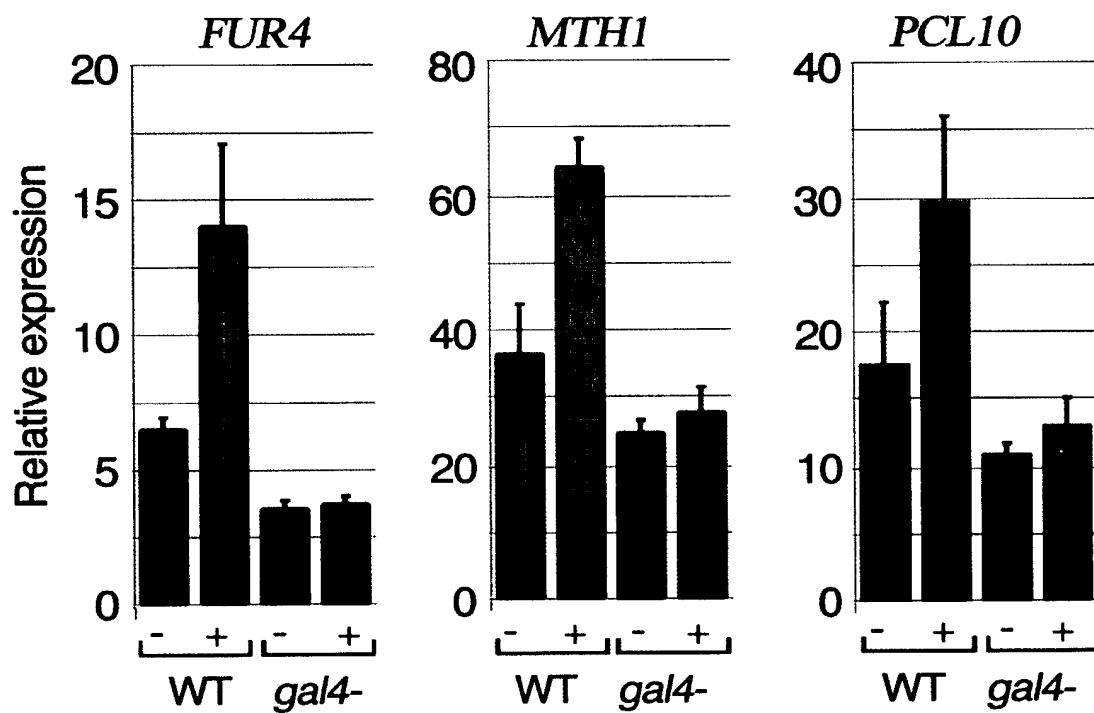
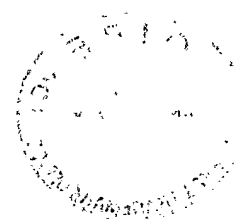


FIGURE 6G



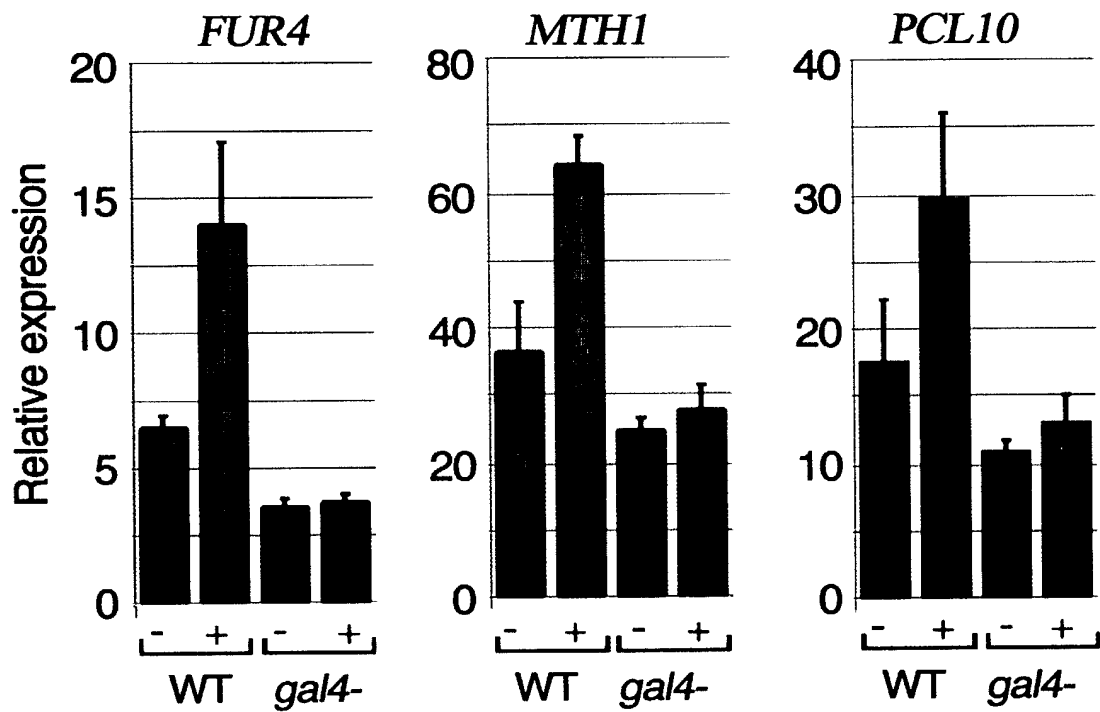


FIGURE 6G



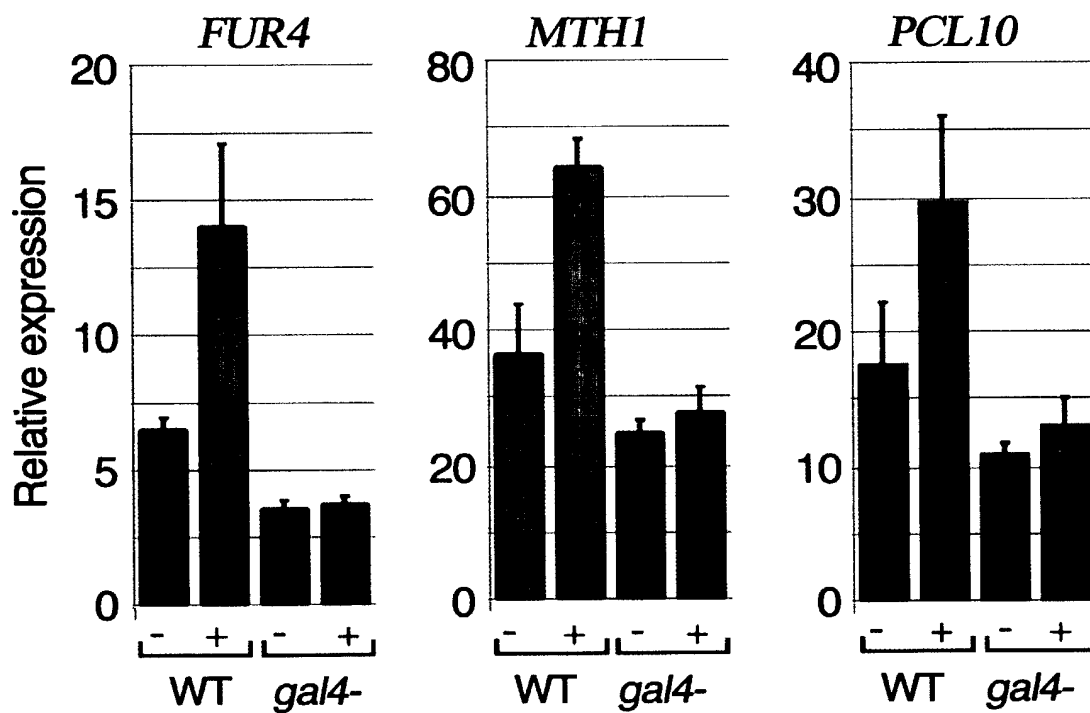
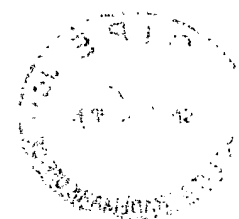


FIGURE 6G



App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

10/032,281

Binding		Expression	Name	Binding		Description
after	before	α-0 α-15 α-30 α-45 α-60 α-90 α-120 Gal:Ste12 Ste12Δ+α		before	after	
				ratio p-value	ratio p-value	
			PRM1	2.7 1.3E-04	6.2 4.5E-05	Pheromone-regulated membrane protein
			ERG24	2.7 1.3E-04	6.2 4.5E-05	C-14 sterol reductase
			PCL2	3.3 4.2E-05	6.8 5.8E-05	Cyclin partly in association with Pho85p
			FIG2	2.6 2.2E-04	5.6 9.5E-05	Protein involved in mating induction
			STE12	4.1 1.4E-06	4.1 3.1E-04	Transcription factor required for mating
			FUS1	5.0 2.8E-07	4.1 5.6E-04	Protein required for cell fusion during mating
			CDC48	2.9 1.5E-04	4.6 1.0E-03	Required for cell division and homotypic membrane fusion
			YCR027C	2.4 5.6E-04	3.2 1.5E-03	Protein involved in growth regulation
			FUS3	3.3 3.9E-05	5.4 2.0E-03	MAPK mediating mating pheromone signaling
			PEP1	3.3 3.9E-05	5.4 2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
			MET2	2.1 4.8E-03	2.8 3.2E-03	Homoserine O-acetyltransferase
			YOR129C	0.7 1.0E+00	5.2 1.0E-04	Protein of unknown function
			UTH1	1.7 2.9E-02	5.2 1.0E-04	Protein involved in the aging process
			AFR1	1.0 8.6E-01	5.1 1.0E-04	Protein involved in morphogenesis of the mating projection
			GIC2	1.4 1.1E-01	5.0 1.2E-04	Putative effector of Cdc42p, important for bud emergence
			YNR046W	1.9 7.6E-03	4.8 1.4E-04	Protein of unknown function
			MSS11	1.0 8.1E-01	4.9 1.8E-04	Protein involved in regulation of starch metabolism
			YOR343C	1.1 7.0E-01	3.9 4.1E-04	Protein of unknown function
			CHS1	0.9 1.0E+00	4.1 4.2E-04	Chitin synthase I, functions during cell separation
			SCH9	1.3 2.1E-01	4.2 4.5E-04	Serine/threonine protein kinase that is activated by cAMP

>5/1 4/1 3/1 2/1 <1:1

>10/1 5/1 2/1 1:1 1/2 1/5 <1/10

>5/1 4/1 3/1 2/1 <1:1 >10/1 5/1 2/1 1:1 1/2 1/5 <1/10

FIGURE 7A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

11032281-060602

Binding		Expression	Name		Binding		Description	
before	after	α-0 α-1.5 α-3.0 α-4.5 α-6.0 α-9.0 α-12.0 Gal:Ste12 Ste12Δ + α	before	after	ratio p-value	ratio p-value		
			PRM1	2.7	1.3E-04	6.2	4.5E-05	Pheromone-regulated membrane protein
			ERG24	2.7	1.3E-04	6.2	4.5E-05	C-14 sterol reductase
			PCL2	3.3	4.2E-05	6.8	5.8E-05	Cyclin partly in association with Pho85p
			FIG2	2.6	2.2E-04	5.6	9.5E-05	Protein involved in mating induction
			STE12	4.1	1.4E-06	4.1	3.1E-04	Transcription factor required for mating
			FUS1	5.0	2.8E-07	4.1	5.6E-04	Protein required for cell fusion during mating
			CDC48	2.9	1.5E-04	4.6	1.0E-03	Required for cell division and homotypic membrane fusion
			YCR027C	2.4	5.6E-04	3.2	1.5E-03	Protein involved in growth regulation
			FUS3	3.3	3.9E-05	5.4	2.0E-03	MAPK mediating mating pheromone signaling
			PEP1	3.3	3.9E-05	5.4	2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
			MET2	2.1	4.8E-03	2.8	3.2E-03	Homoserine O-acetyltransferase
			YOR129C	0.7	1.0E+00	5.2	1.0E-04	Protein of unknown function
			UTH1	1.7	2.9E-02	5.2	1.0E-04	Protein involved in the aging process
			AFR1	1.0	8.6E-01	5.1	1.0E-04	Protein involved in morphogenesis of the mating projection
			GIC2	1.4	1.1E-01	5.0	1.2E-04	Putative effector of Cdc42p, important for bud emergence
			YNR046W	1.9	7.6E-03	4.8	1.4E-04	Protein of unknown function
			MSS11	1.0	8.1E-01	4.9	1.8E-04	Protein involved in regulation of starch metabolism
			YOR343C	1.1	7.0E-01	3.9	4.1E-04	Protein of unknown function
			CHS1	0.9	1.0E+00	4.1	4.2E-04	Chitin synthase I, functions during cell separation
			SCH9	1.3	2.1E-01	4.2	4.5E-04	Serine/threonine protein kinase that is activated by cAMP

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FIGURE 7A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

Binding		Expression	Name	Binding		Description
before	after	Gal:ste12 a-120 a-90 a-60 a-45 a-30 a-15 a-0		before	after	
				ratio p-value	ratio p-value	
		Ste12 Δ + α	PRM1	2.7 1.3E-04	6.2 4.5E-05	Pheromone-regulated membrane protein
		Gal:ste12	ERG24	2.7 1.3E-04	6.2 4.5E-05	C-14 sterol reductase
			PCL2	3.3 4.2E-05	6.8 5.8E-05	Cyclin partly in association with Pho85p
			FIG2	2.6 2.2E-04	5.6 9.5E-05	Protein involved in mating induction
			STE12	4.1 1.4E-06	4.1 3.1E-04	Transcription factor required for mating
			FUS1	5.0 2.8E-07	4.1 5.6E-04	Protein required for cell fusion during mating
			CDC48	2.9 1.5E-04	4.6 1.0E-03	Required for cell division and homotypic membrane fusion
			YCR027C	2.4 5.6E-04	3.2 1.5E-03	Protein involved in growth regulation
			FUS3	3.3 3.9E-05	5.4 2.0E-03	MAPK mediating mating pheromone signaling
			PEP1	3.3 3.9E-05	5.4 2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
			MET2	2.1 4.8E-03	2.8 3.2E-03	Homoserine O-acetyltransferase
			YOR129C	0.7 1.0E+00	5.2 1.0E-04	Protein of unknown function
			UTH1	1.7 2.9E-02	5.2 1.0E-04	Protein involved in the aging process
			AFR1	1.0 8.6E-01	5.1 1.0E-04	Protein involved in morphogenesis of the mating projection
			GIC2	1.4 1.1E-01	5.0 1.2E-04	Putative effector of Cdc42p, important for bud emergence
			YNR046W	1.9 7.6E-03	4.8 1.4E-04	Protein of unknown function
			MSS11	1.0 8.1E-01	4.9 1.8E-04	Protein involved in regulation of starch metabolism
			YOR343C	1.1 7.0E-01	3.9 4.1E-04	Protein of unknown function
			CHS1	0.9 1.0E+00	4.1 4.2E-04	Chitin synthase I, functions during cell separation
			SCH9	1.3 2.1E-01	4.2 4.5E-04	Serine/threonine protein kinase that is activated by cAMP

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FIGURE 7A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

Binding	Expression	Name	Binding		Description		
			before	after			
after	before		ratio	p-value	ratio	p-value	
		PRM1	2.7	1.3E-04	6.2	4.5E-05	Pheromone-regulated membrane protein
		ERG24	2.7	1.3E-04	6.2	4.5E-05	C-14 sterol reductase
		PCL2	3.3	4.2E-05	6.8	5.8E-05	Cyclin partly in association with Pho85p
		FIG2	2.6	2.2E-04	5.6	9.5E-05	Protein involved in mating induction
		STE12	4.1	1.4E-06	4.1	3.1E-04	Transcription factor required for mating
		FUS1	5.0	2.8E-07	4.1	5.6E-04	Protein required for cell fusion during mating
		CDC48	2.9	1.5E-04	4.6	1.0E-03	Required for cell division and homotypic membrane fusion
		YCR027C	2.4	5.6E-04	3.2	1.5E-03	Protein involved in growth regulation
		FUS3	3.3	3.9E-05	5.4	2.0E-03	MAPK mediating mating pheromone signaling
		PEP1	3.3	3.9E-05	5.4	2.0E-03	Receptor for vacuolar sorting of soluble vacuolar proteins
		MET2	2.1	4.8E-03	2.8	3.2E-03	Homoserine O-acetyltransferase
		YOR129C	0.7	1.0E+00	5.2	1.0E-04	Protein of unknown function
		UTH1	1.7	2.9E-02	5.2	1.0E-04	Protein involved in the aging process
		AFR1	1.0	8.6E-01	5.1	1.0E-04	Protein involved in morphogenesis of the mating projection
		GIC2	1.4	1.1E-01	5.0	1.2E-04	Putative effector of Cdc42p, important for bud emergence
		YNR046W	1.9	7.6E-03	4.8	1.4E-04	Protein of unknown function
		MSS11	1.0	8.1E-01	4.9	1.8E-04	Protein involved in regulation of starch metabolism
		YOR343C	1.1	7.0E-01	3.9	4.1E-04	Protein of unknown function
		CHS1	0.9	1.0E+00	4.1	4.2E-04	Chitin synthase I, functions during cell separation
		SCH9	1.3	2.1E-01	4.2	4.5E-04	Serine/threonine protein kinase that is activated by cAMP

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FIGURE 7A

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

10/032,281 - 06/05/02

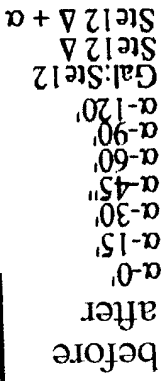
Binding	Expression	Name	Binding		ratio	p-value	Description
			before	after			
	before						
	after						
	α -0						
	α -15						
	α -30						
	α -45						
	α -60						
	α -90						
	α -120						
	Gal:Ste12						
	Ste12 Δ						
	Ste12 Δ + α						
		KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion
		YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function
		YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function
		SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body
		YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases
		YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function
		PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucosyltransferase
		YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function
		YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function
		AGA1	1.4	1.1E-01	3.1	1.9E-03	a-Agglutinin anchor subunit
		YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to S. cerevisiae glucan 1,4-alpha-glucosidase
		VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog
		CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy
		FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating
		PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex
		YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to Rhodobacter capsulatus bchO protein
		HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to Aspergillus nidulans hymA
		FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating

FIGURE 7B

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

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Binding	Expression	Name	Binding		Description		
			before	after			
			ratio	p-value			
α-0	α-0	KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion
α-15	α-15	YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function
α-30	α-30	YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function
α-45	α-45	SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body
α-60	α-60	YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases
α-90	α-90	YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function
α-120	α-120	PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucomutase
Gal:Ste12	Gal:Ste12	YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function
Ste12Δ	Ste12Δ	YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function
Ste12Δ + α	Ste12Δ + α	AGA1	1.4	1.1E-01	3.1	1.9E-03	α-Agglutinin anchor subunit
		YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to S. cerevisiae glucan 1,4-α-glucosidase
		VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog
		CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy
		FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating
		PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex
		YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to Rhodobacter capsulatus bchO protein
		HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to Aspergillus nidulans hymA
		FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating

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FIGURE 7B

FIGURE 7B

Binding	Expression	Name	Binding		Description		
			before	after			
after	α-0		ratio	p-value			
before	α-15		ratio	p-value			
	α-30		ratio	p-value			
	α-45		ratio	p-value			
	α-60		ratio	p-value			
	α-90		ratio	p-value			
	α-120		ratio	p-value			
	Gal:Ste12		ratio	p-value			
	Ste12Δ		ratio	p-value			
	Ste12Δ + α		ratio	p-value			
		KAR5	1.2	3.7E-01	3.8	4.7E-04	Membrane protein required for homotypic nuclear fusion
		YER048W-A	1.5	1.0E-01	3.8	5.1E-04	Protein of unknown function
		YPL192C	0.9	1.0E+00	3.6	6.5E-04	Protein of unknown function
		SPC25	1.3	2.0E-01	4.1	6.6E-04	Protein of the spindle pole body
		YER019W	1.3	2.0E-01	4.1	6.6E-04	Moderately similar to mammalian neutral sphingomyelinases
		YIL083C	1.0	6.7E-01	3.6	7.1E-04	Protein of unknown function
		PGM1	2.0	6.1E-03	3.8	7.2E-04	Phosphoglucomutase
		YIL037C	1.1	5.5E-01	3.4	8.2E-04	Protein of unknown function
		YIL169C	1.6	7.2E-02	3.3	1.2E-03	Protein of unknown function
		AGA1	1.4	1.1E-01	3.1	1.9E-03	α-Agglutinin anchor subunit
		YOL155C	1.0	7.3E-01	3.0	2.1E-03	Similar to <i>S. cerevisiae</i> glucan 1,4-α-glucosidase
		VTI1	0.9	1.0E+00	3.0	2.2E-03	Synaptobrevin (v-SNARE) homolog
		CIK1	0.9	1.0E+00	3.0	2.2E-03	Involved in spindle formation and karyogamy
		FAR1	1.3	2.2E-01	3.0	2.4E-03	Involved in cell cycle arrest for mating
		PHO81	1.0	8.3E-01	2.9	2.7E-03	CDK inhibitor for Pho80p-Pho85p complex
		YNR064C	1.5	7.4E-02	2.7	4.5E-03	Similar to <i>Rhodobacter capsulatus</i> bchO protein
		HYM1	1.4	1.8E-01	2.7	4.9E-03	Protein with similarity to <i>Aspergillus nidulans</i> hymA
		FIG1	1.2	3.8E-01	2.9	5.0E-03	Protein required for efficient mating

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FIGURE 7B

App No.: 10/032,281

10032281_050602

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

Binding	Expression	Name	Binding		ratio	p-value	Description
			before	after			
		BMH2	2.1	3.2E-03	4.1	6.5E-04	Homolog to 14-3-3 protein; adjacent to Ty element YDRCdelta9
		YGR189C	1.7	2.4E-02	4.8	1.7E-04	Cell wall protein; adjacent to TY element YGRWdelta31
		YNR053C	1.9	9.7E-03	4.3	2.6E-04	Unknown function; adjacent to Ty element YNRWsigma4
		MSO1	1.9	1.8E-02	4.3	2.9E-04	Multicopy suppressor of sec1; adjacent to Ty element YNRWsigma4
		TYE7	1.0	1.0E+00	3.9	4.6E-04	Basic helix-loop-helix transcription factor
		YNR051C	1.8	1.4E-02	3.8	4.7E-04	Similar to chicken nucleolin; adjacent to Ty element YNRWsigma4
		YNR048W	1.9	9.2E-03	3.9	4.9E-04	Protein of unknown function; adjacent to Ty element YNRWsigma4
		YGL050W	1.7	2.0E-02	3.8	5.1E-04	Protein of unknown function; adjacent to Ty element YGLCsigma3
		YIL036W	1.1	5.5E-01	3.4	8.2E-04	Similar to Mei4p and to CREB proteins; adjacent to YIL037C
		YNR067C	2.0	1.3E-02	3.4	1.1E-03	Protein of unknown function
		SDL1	1.6	7.2E-02	3.3	1.2E-03	Serine dehydratase; adjacent to YIL169C
		YDR281C	1.2	4.2E-01	3.1	1.7E-03	Protein of unknown function; adjacent to Ty element YDRWsigma5
		YDR100W	1.1	3.6E-01	5.5	1.9E-03	Protein of unknown function; adjacent to Ty element YDRCdelta9
		YNL043C	1.1	5.7E-01	3.0	2.1E-03	Protein of unknown function; adjacent to Ty element YNLWsigma2
		YOL154W	1.0	7.3E-01	3.0	2.1E-03	Similar to Zinc metalloproteinases; adjacent to YOL155C
		YHB1	1.0	8.3E-01	2.9	2.7E-03	Flavohemoglobin of unknown function; adjacent to PHO81
		PAN3	1.8	6.5E-02	4.6	3.5E-03	Component of Pab1p-stimulated poly(A) ribonuclease
		CWP2	1.8	1.5E-02	2.8	3.6E-03	major constituent of the cell wall containing GPI-anchor
		YKL097C	1.8	1.5E-02	2.8	3.6E-03	Protein of unknown function; adjacent to CWP2

FIGURE 7C

Binding	Expression	Name	Binding		Description
			before	after	
			ratio	p-value	
after	before				
0-0	0-0	BMH2	2.1	3.2E-03	4.1 6.5E-04 Homolog to 14-3-3 protein; adjacent to Ty element YDRCdelta9
0-15	0-15	YGR189C	1.7	2.4E-02	4.8 1.7E-04 Cell wall protein; adjacent to Ty element YGRWdelta31
0-30	0-30	YNR053C	1.9	9.7E-03	4.3 2.6E-04 Unknown function; adjacent to Ty element YNRWsigma4
0-45	0-45	MSO1	1.9	1.8E-02	4.3 2.9E-04 Multicopy suppressor of sec1; adjacent to Ty element YNRWsigma4
0-60	0-60	TYE7	1.0	1.0E+00	3.9 4.6E-04 Basic helix-loop-helix transcription factor
0-90	0-90	YNR051C	1.8	1.4E-02	3.8 4.7E-04 Similar to chicken nucleolin; adjacent to Ty element YNRWsigma4
0-120	0-120	YNR048W	1.9	9.2E-03	3.9 4.9E-04 Protein of unknown function; adjacent to Ty element YNRWsigma4
Gal:Ste12	Gal:Ste12	YGL050W	1.7	2.0E-02	3.8 5.1E-04 Protein of unknown function; adjacent to Ty element YGLCsigma3
Ste12Δ + α	Ste12Δ + α	YIL036W	1.1	5.5E-01	3.4 8.2E-04 Similar to Mei4p and to CREB proteins; adjacent to YIL037C
		YNR067C	2.0	1.3E-02	3.4 1.1E-03 Protein of unknown function
		SDL1	1.6	7.2E-02	3.3 1.2E-03 Serine dehydratase; adjacent to YIL169C
		YDR281C	1.2	4.2E-01	3.1 1.7E-03 Protein of unknown function; adjacent to Ty element YDRWsigma5
		YDR100W	1.1	3.6E-01	5.5 1.9E-03 Protein of unknown function; adjacent to Ty element YDRCdelta9
		YNL043C	1.1	5.7E-01	3.0 2.1E-03 Protein of unknown function; adjacent to Ty element YNLWsigma2
		YOL154W	1.0	7.3E-01	3.0 2.1E-03 Similar to Zinc metalloproteinases; adjacent to YOL155C
		YHB1	1.0	8.3E-01	2.9 2.7E-03 Flavohemoglobin of unknown function; adjacent to PHO81
		PAN3	1.8	6.5E-02	4.6 3.5E-03 Component of Pab1p-stimulated poly(A) ribonuclease
		CWP2	1.8	1.5E-02	2.8 3.6E-03 major constituent of the cell wall containing GPI-anchor
		YKL097C	1.8	1.5E-02	2.8 3.6E-03 Protein of unknown function; adjacent to CWP2

FIGURE 7C

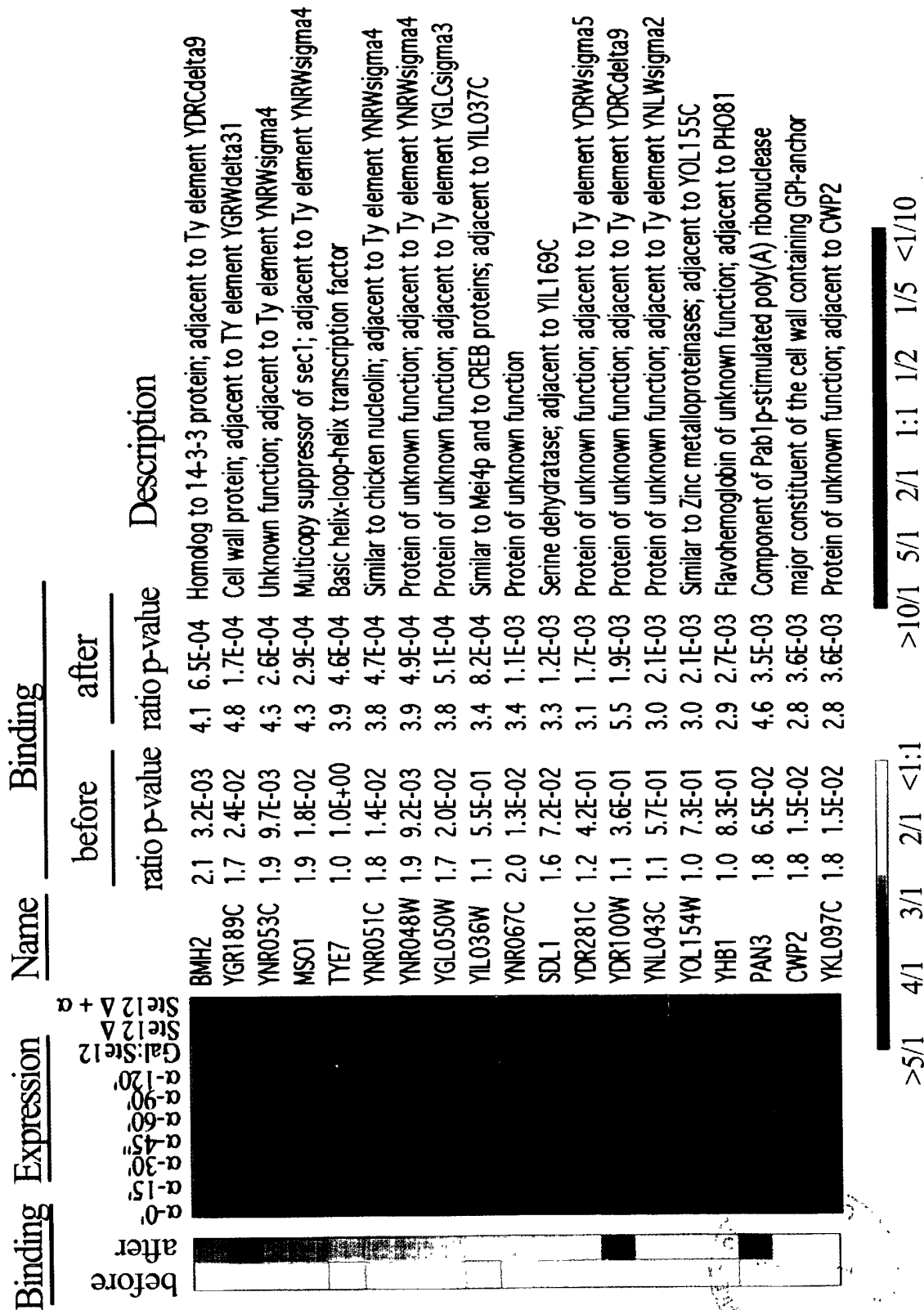


FIGURE 7C

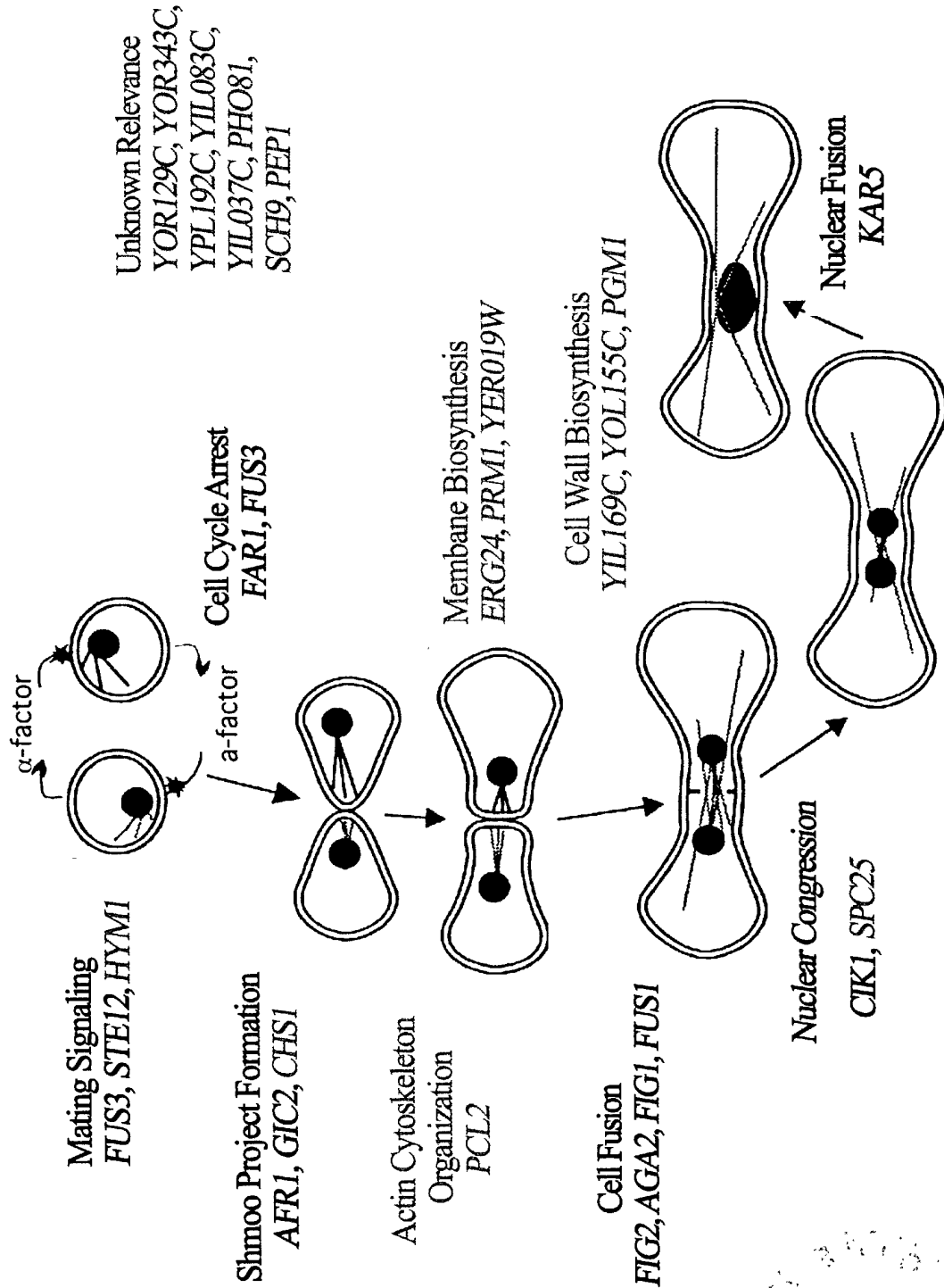


FIGURE 8

App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

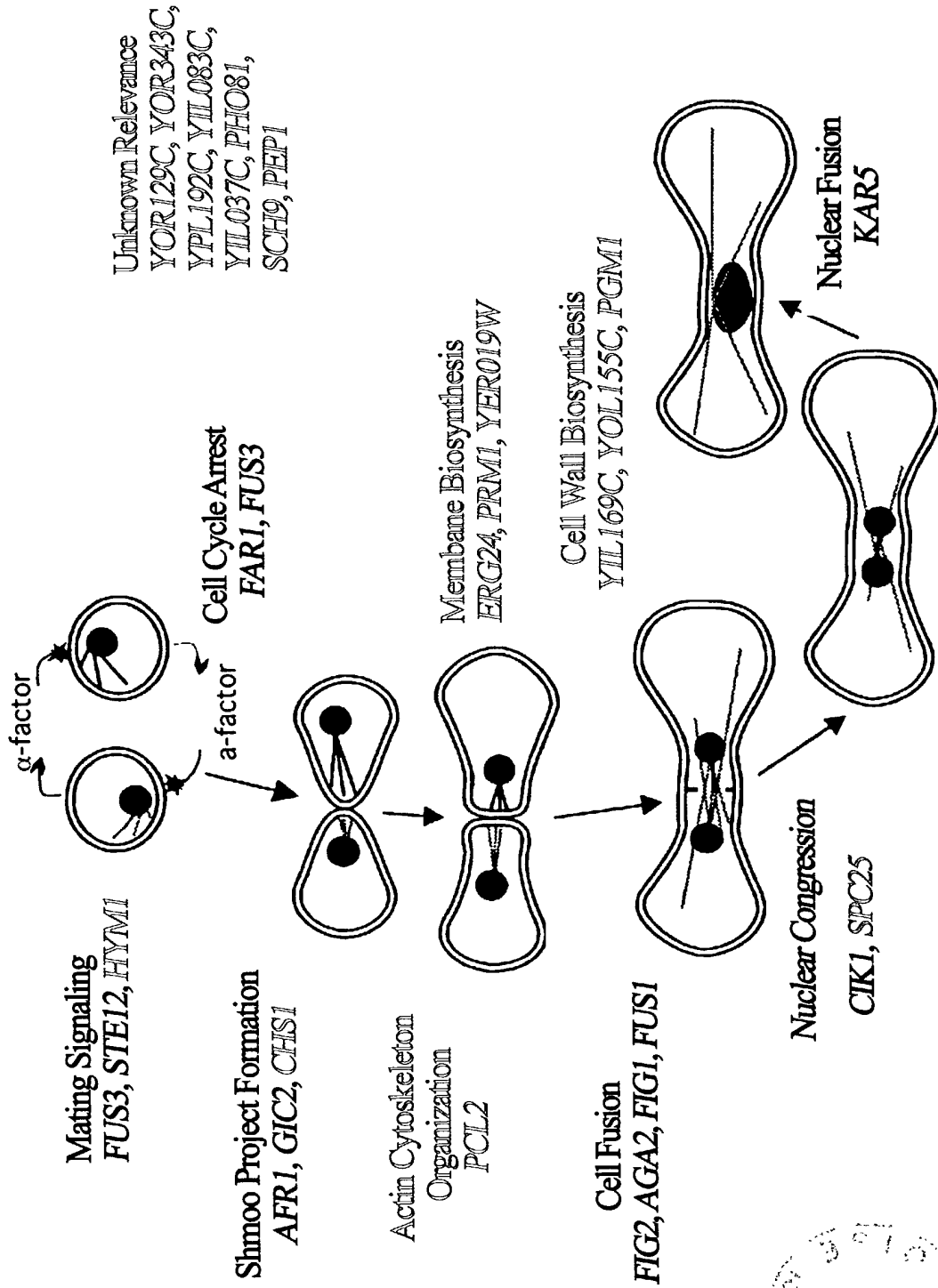


FIGURE 8

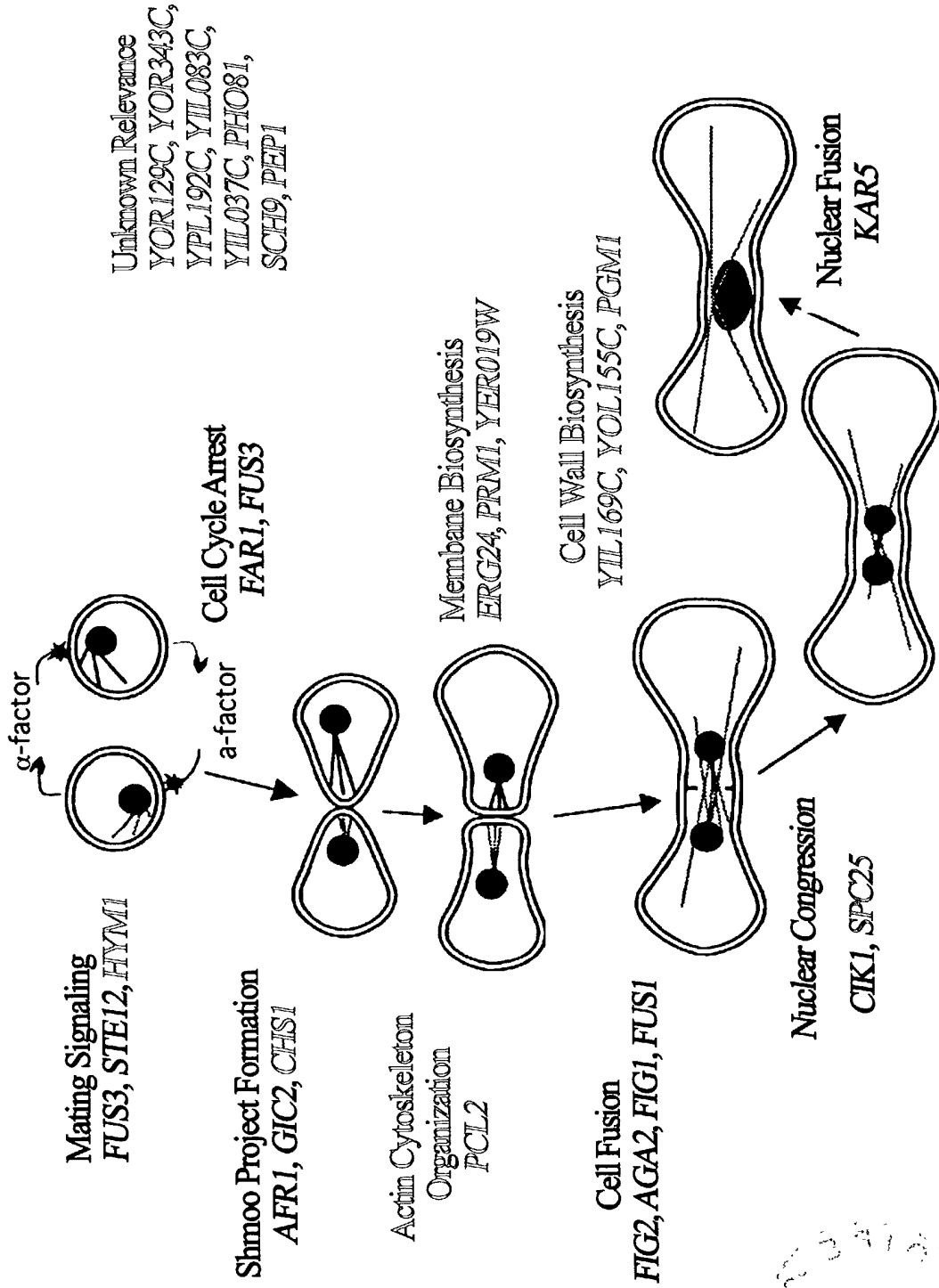


FIGURE 8

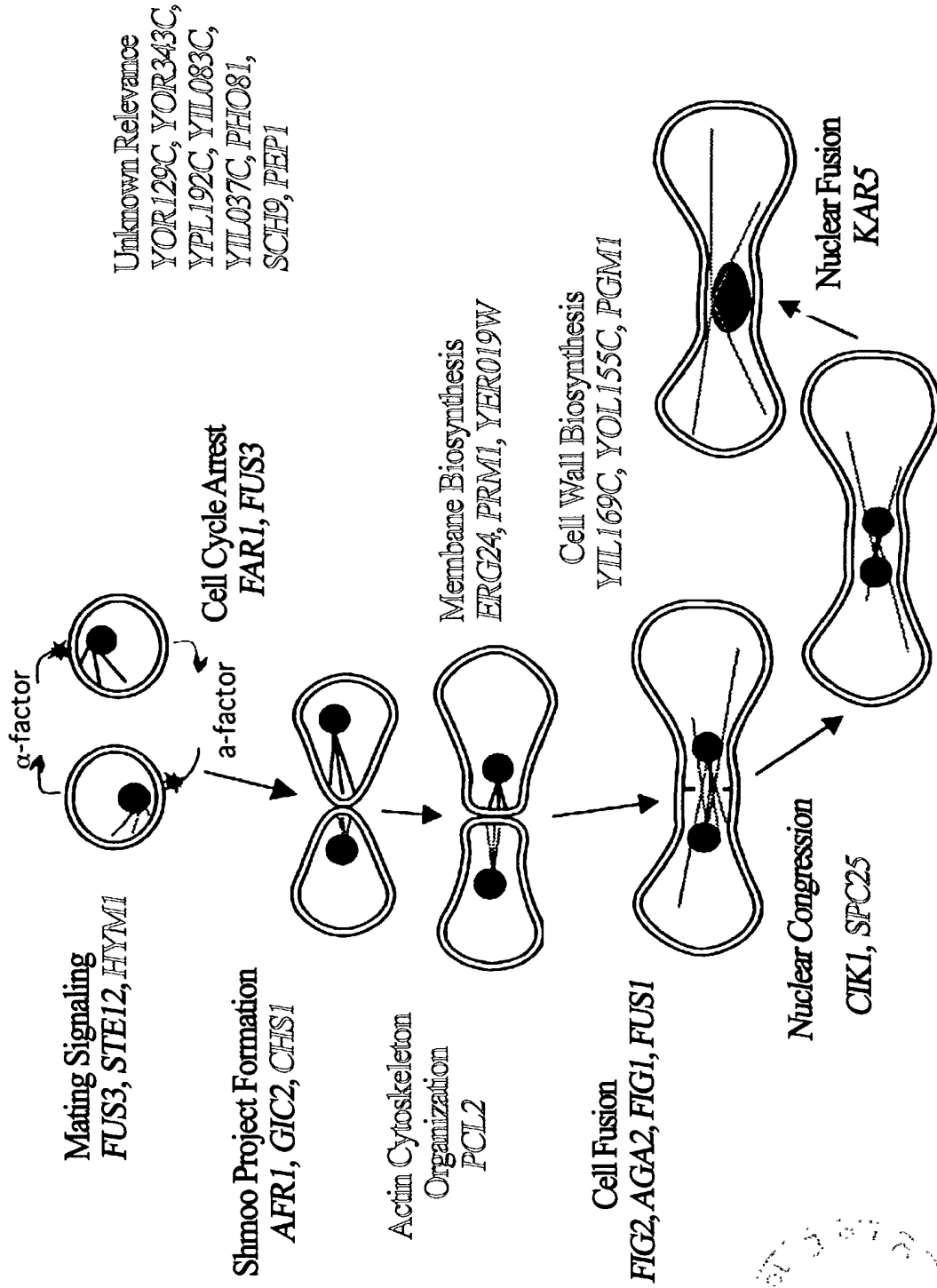


FIGURE 8

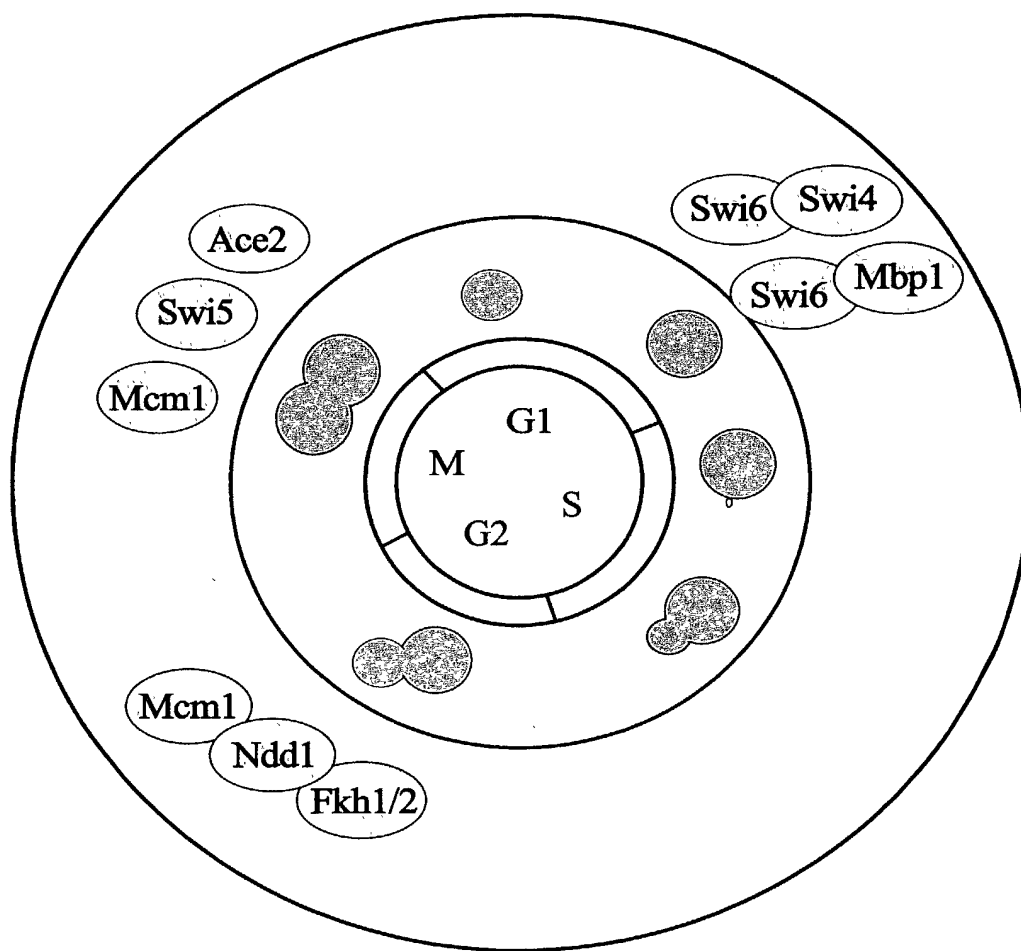


FIGURE 9A



App No.: 10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

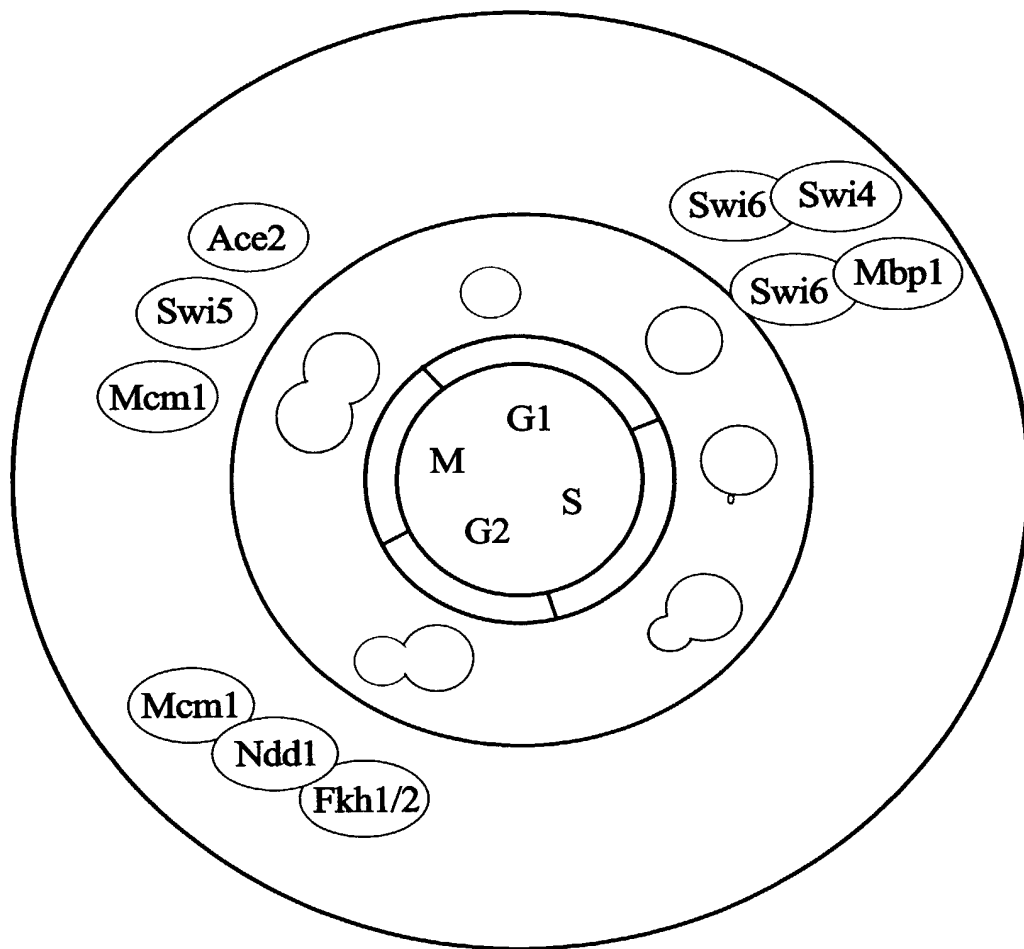
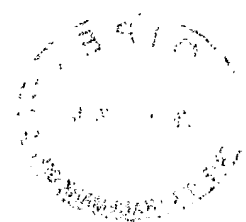


FIGURE 9A



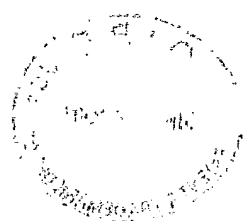


FIGURE 9A

App No.: 10/032,281

10/032,281

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

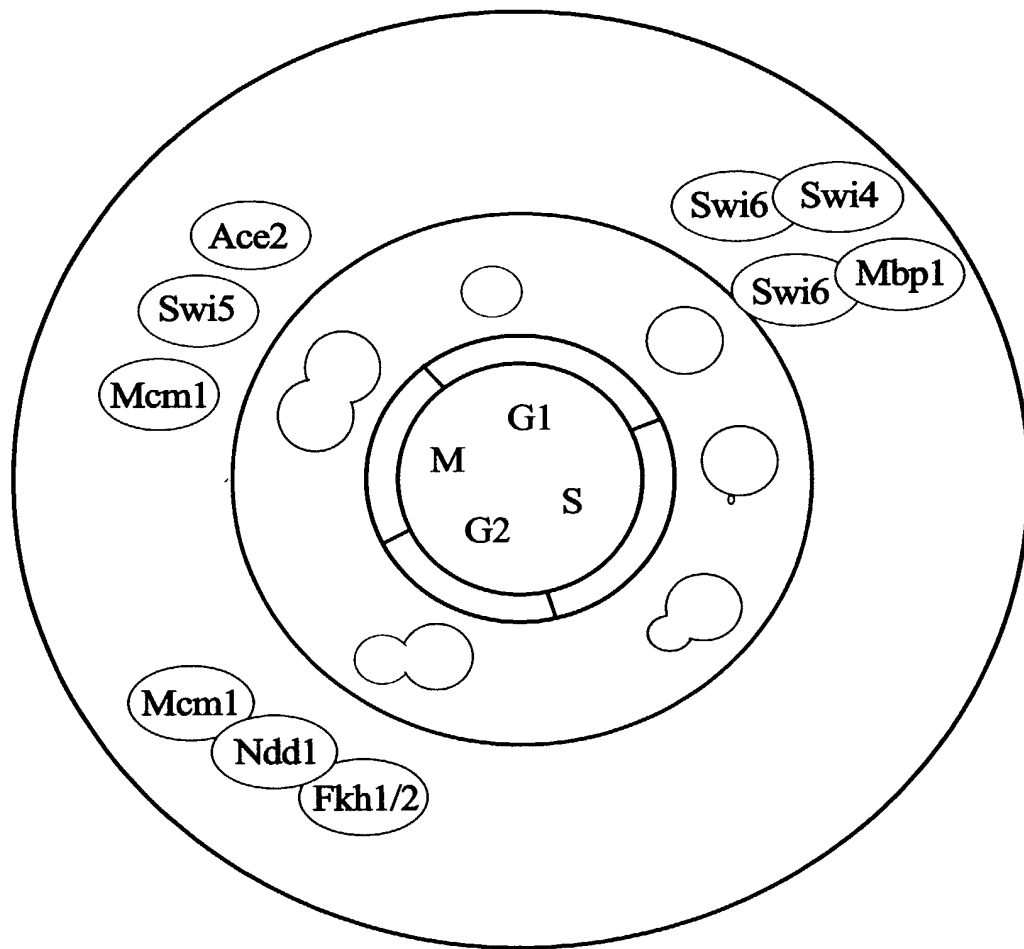


FIGURE 9A



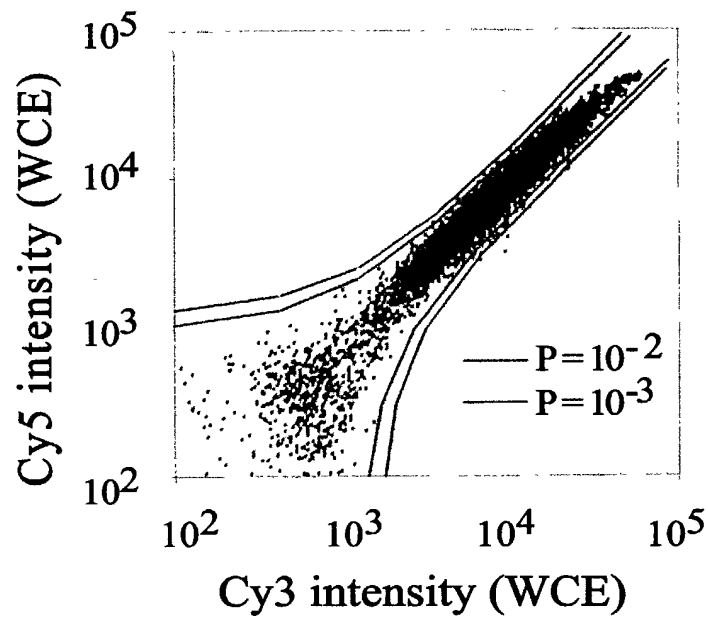


FIGURE 9B

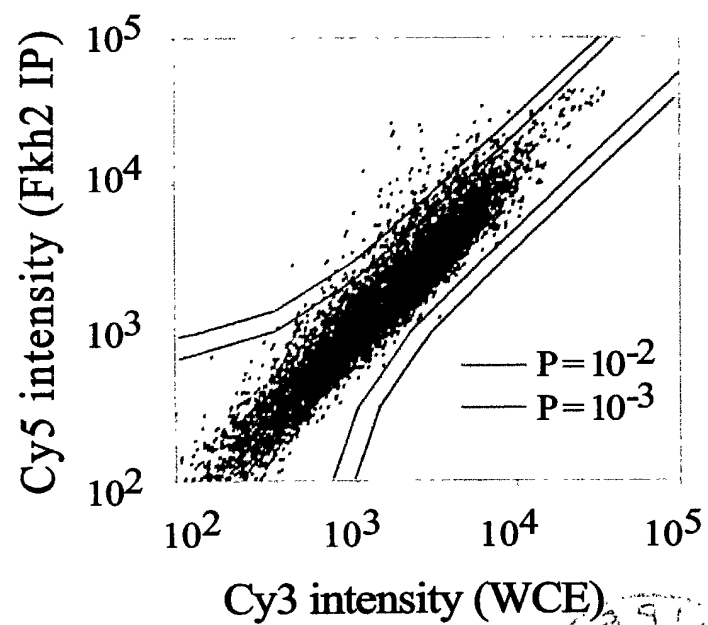


FIGURE 9C



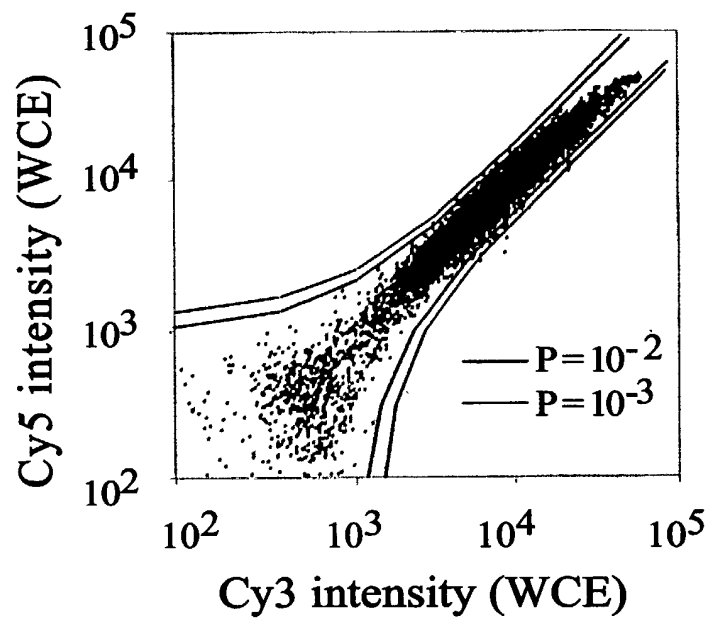


FIGURE 9B

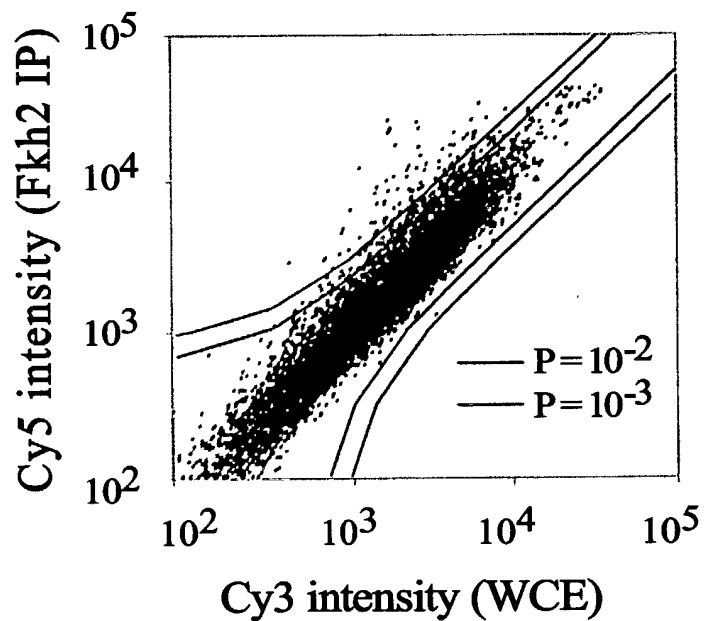


FIGURE 9C



App No.: 10/032,281

10/032,281 - 060902

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

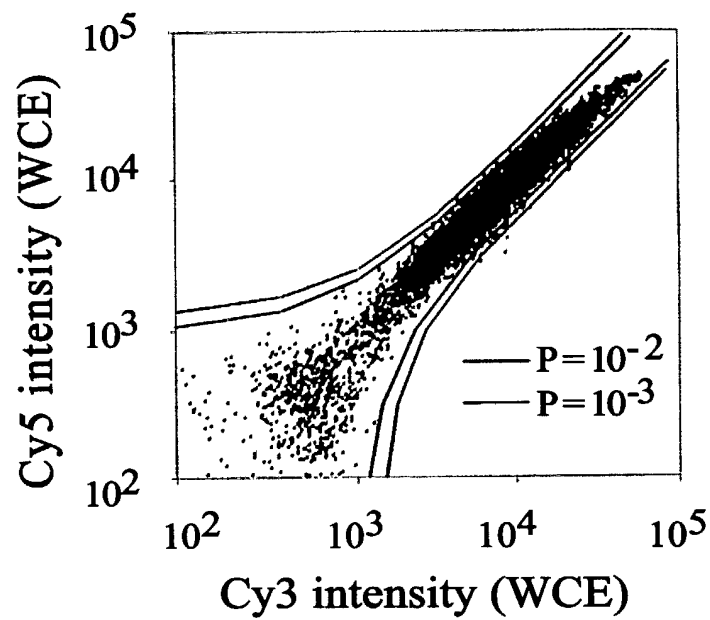


FIGURE 9B

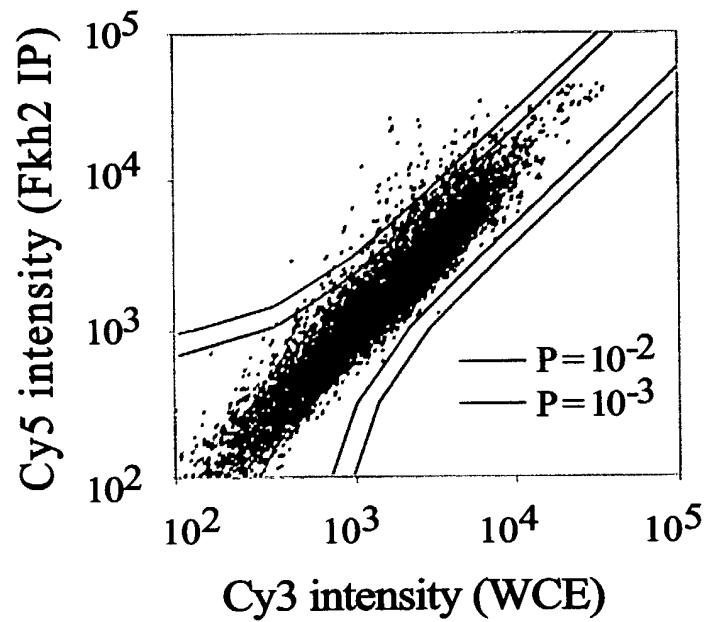


FIGURE 9C



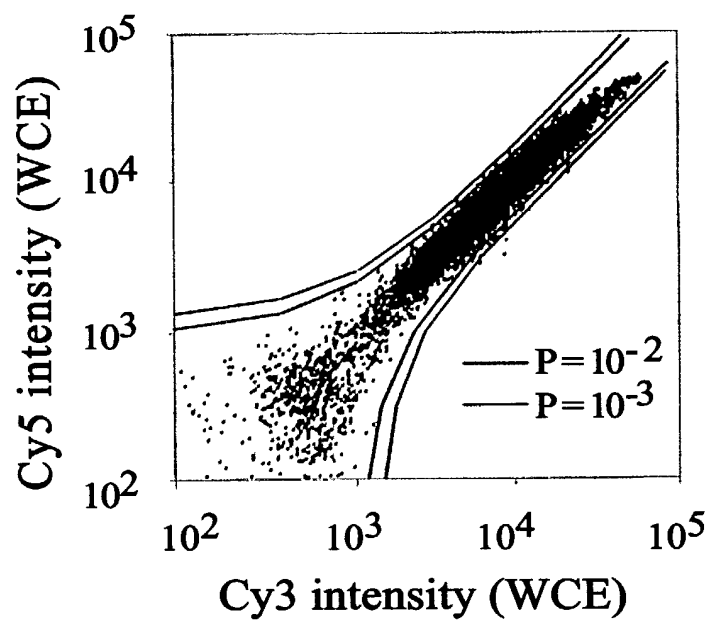


FIGURE 9B

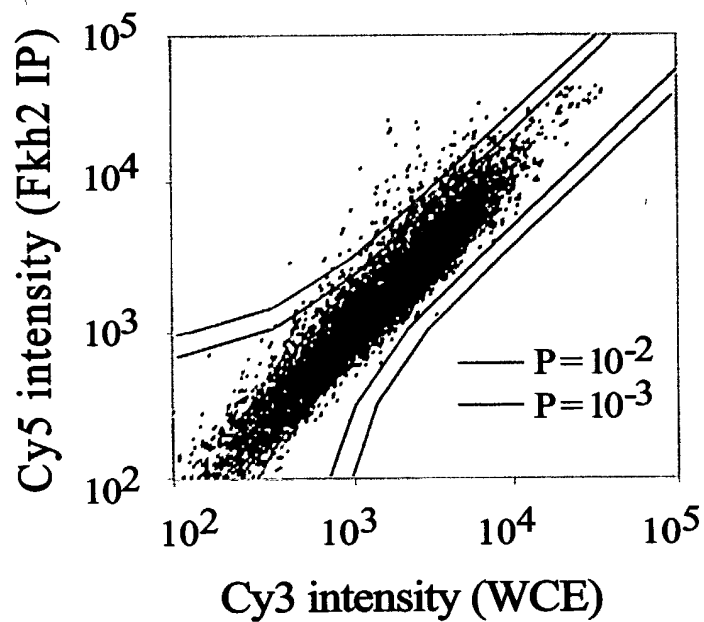


FIGURE 9C



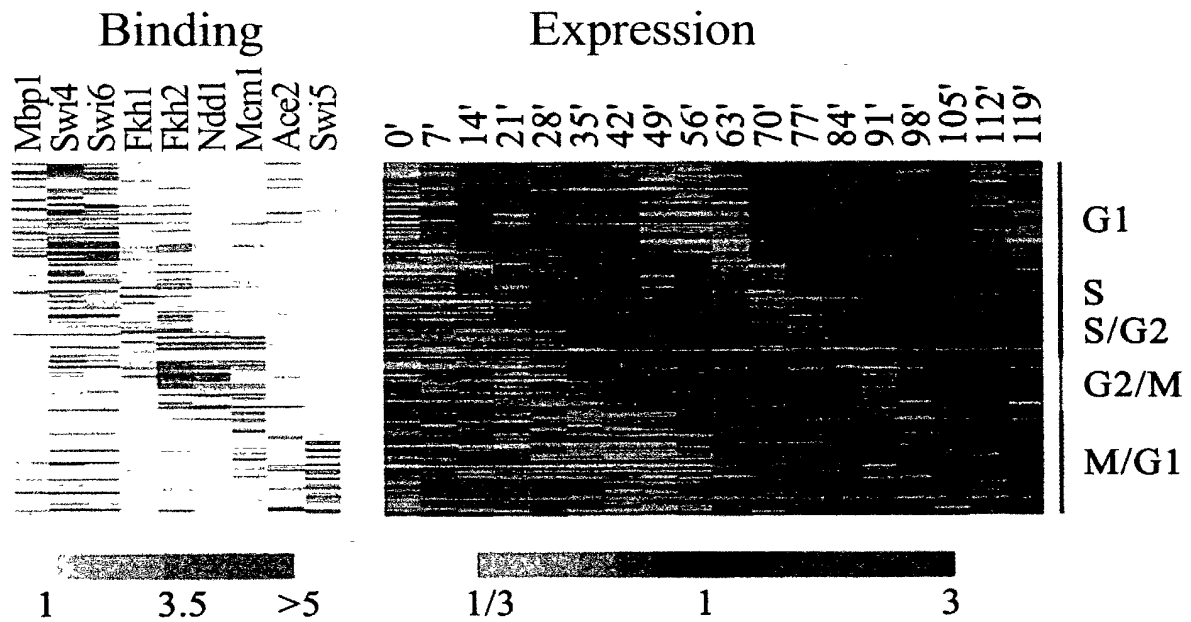


FIGURE 10A

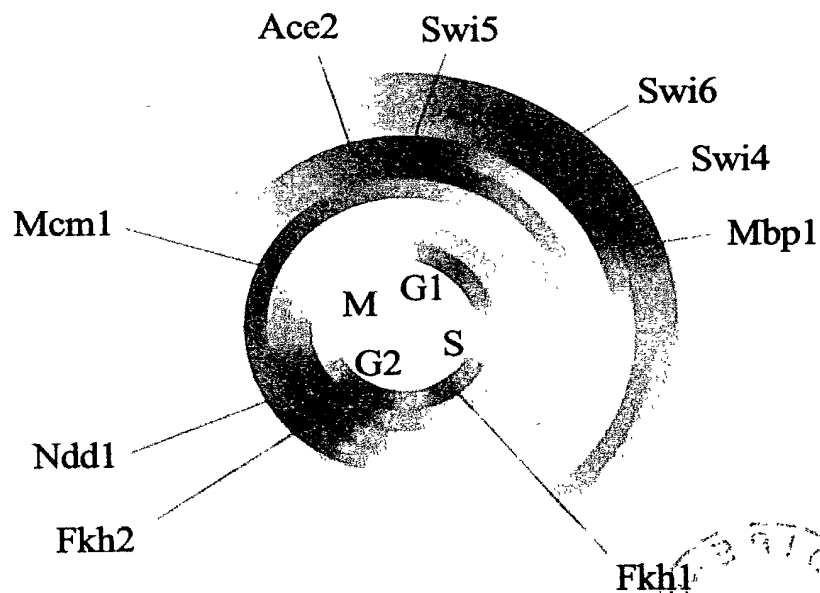


FIGURE 10B

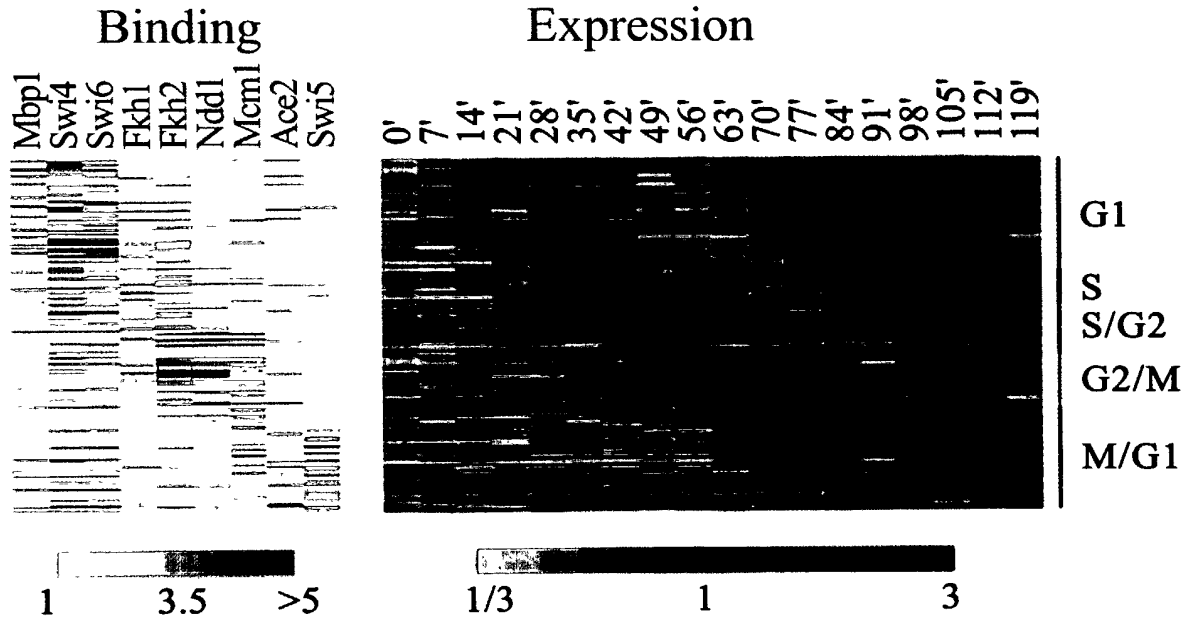


FIGURE 10A

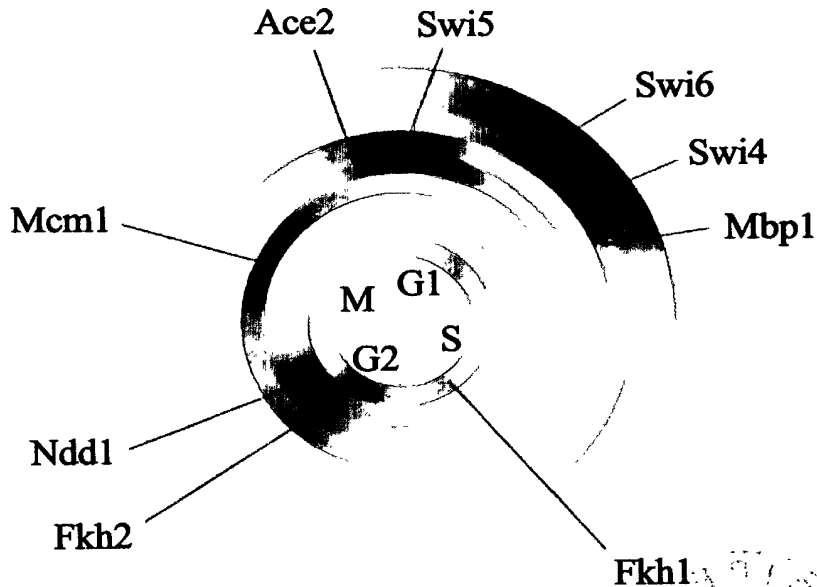


FIGURE 10B

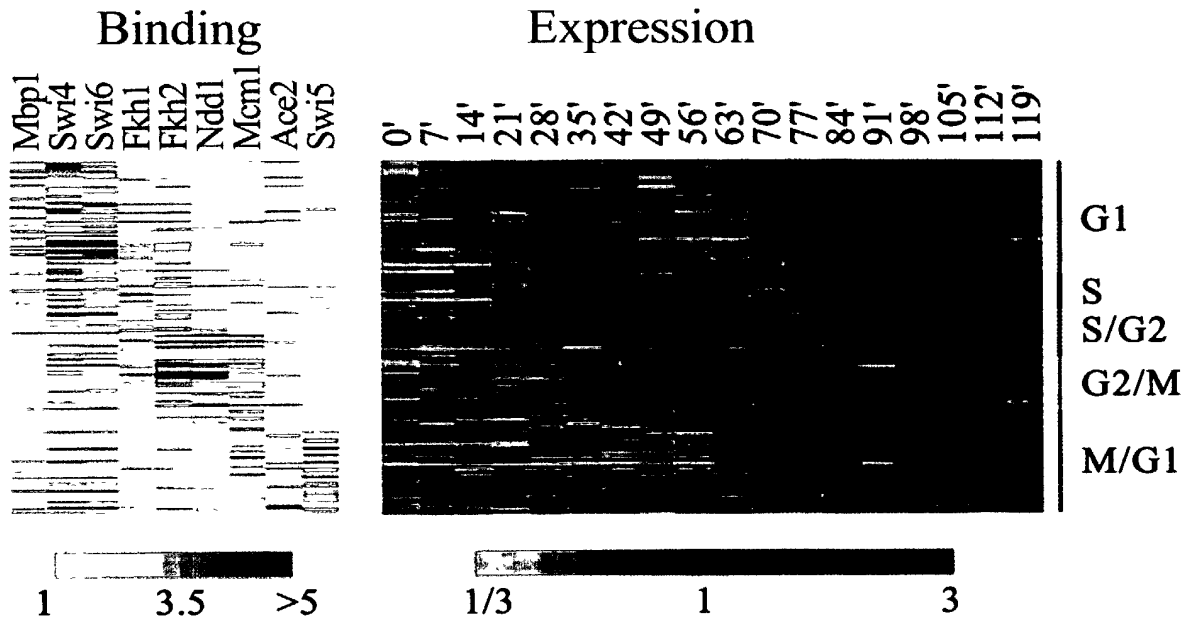


FIGURE 10A

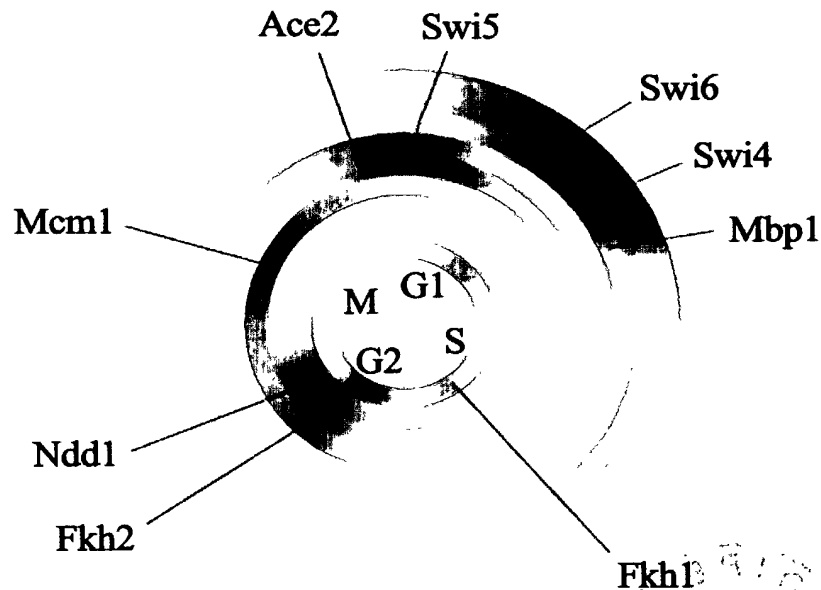


FIGURE 10B

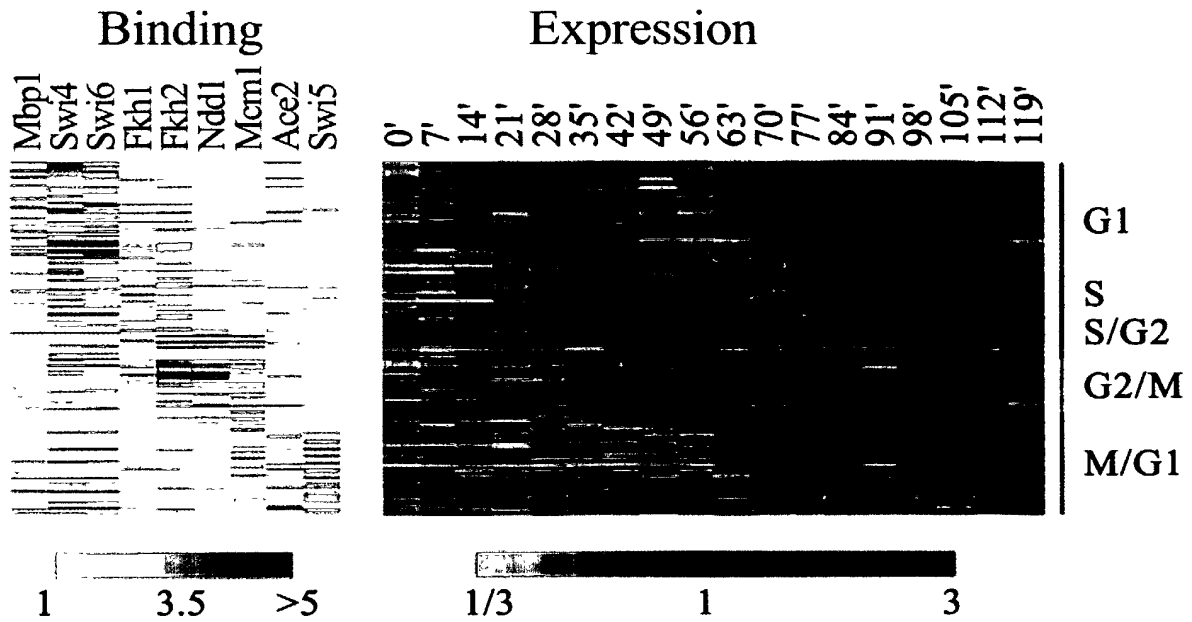


FIGURE 10A

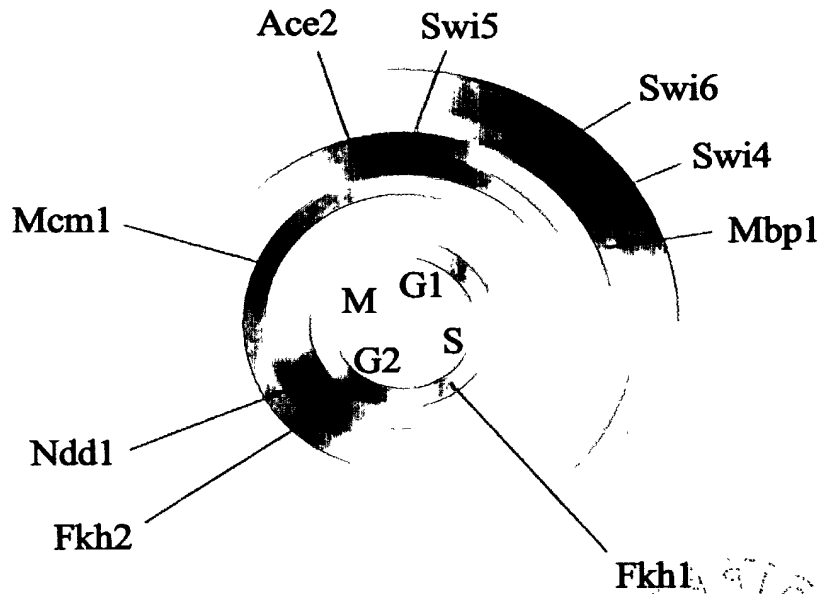


FIGURE 10B

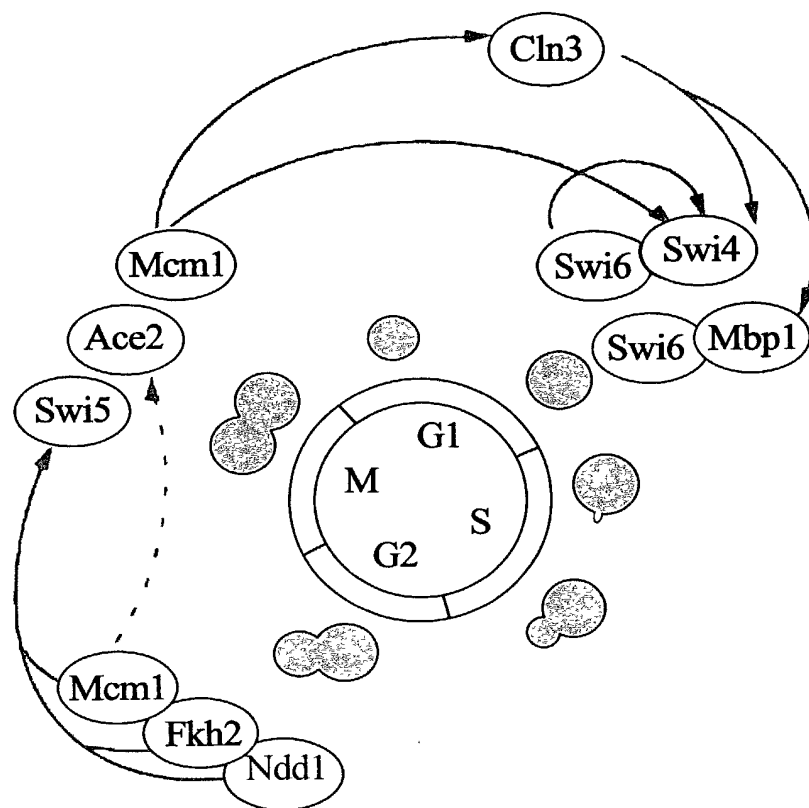


FIGURE 11A



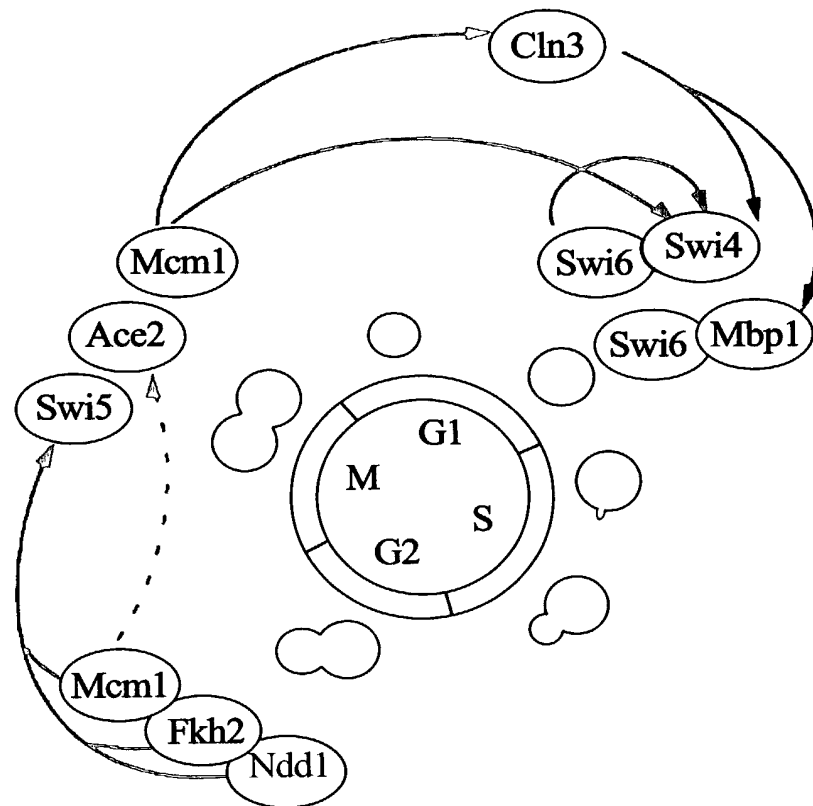


FIGURE 11A



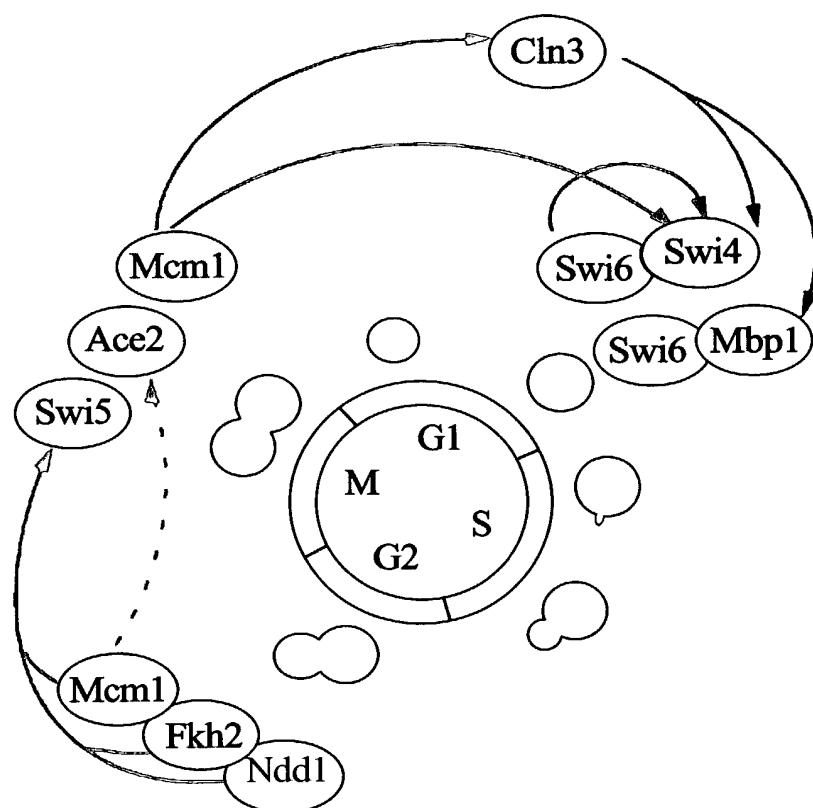
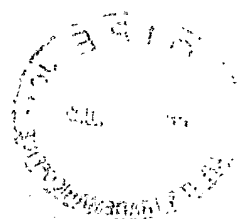


FIGURE 11A



App No.: 10/032,281

Pub. No. 2006/016062

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

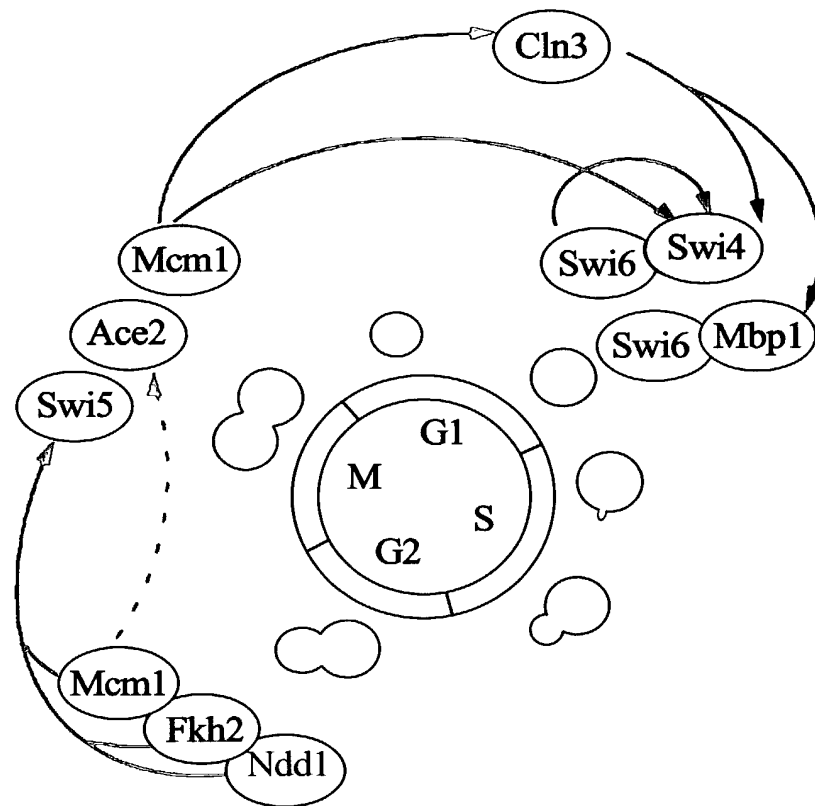


FIGURE 11A



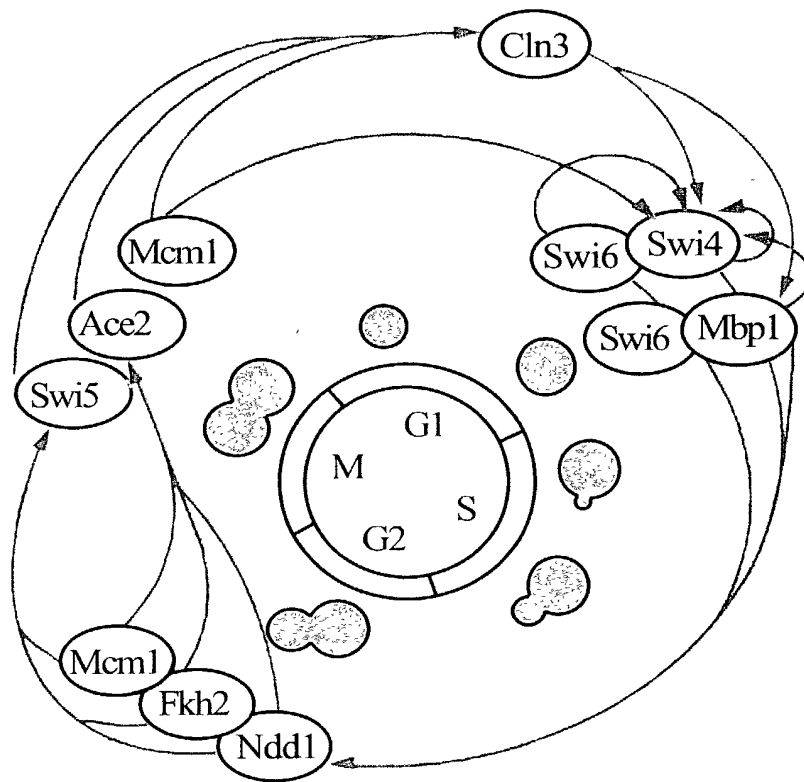


FIGURE 11B



App No.: 10/032,281

3706793 1061062

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

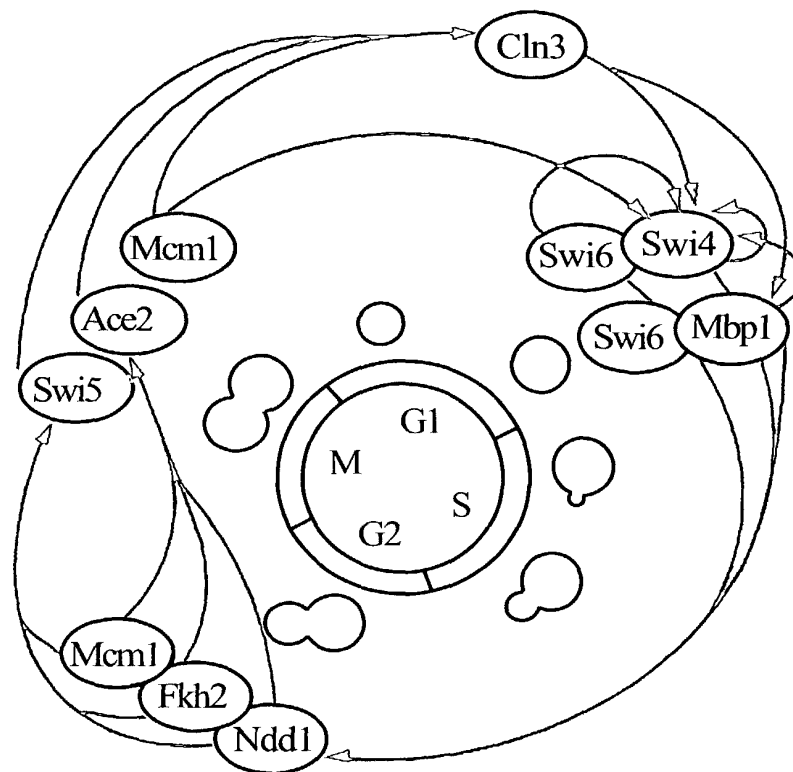


FIGURE 11B

3706793 1061062

App No.: 10/032,281

10/032,281 US 06,062

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

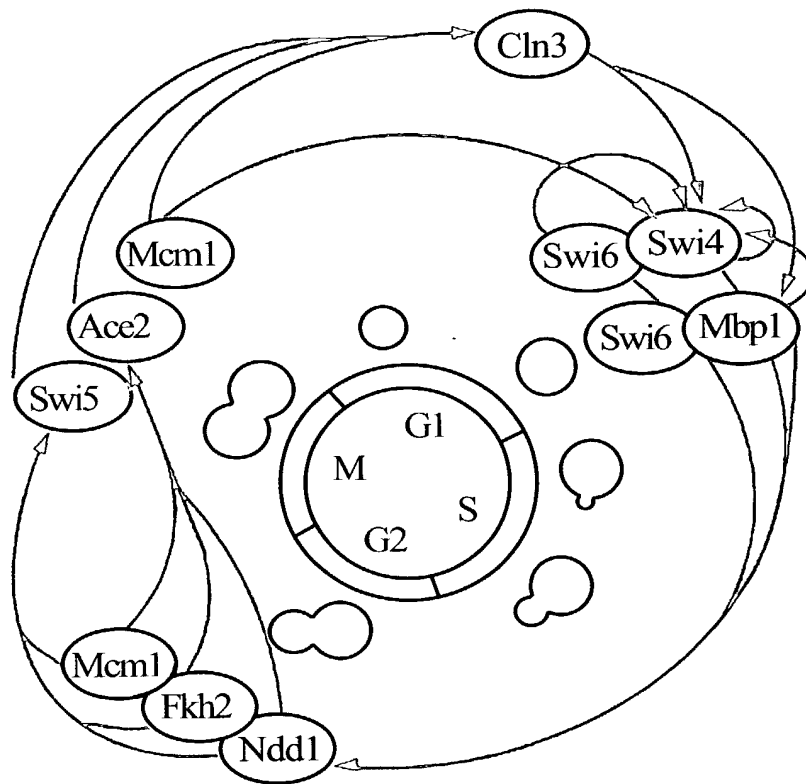
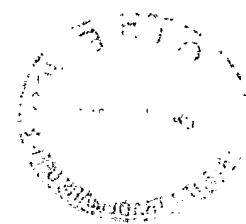


FIGURE 11B



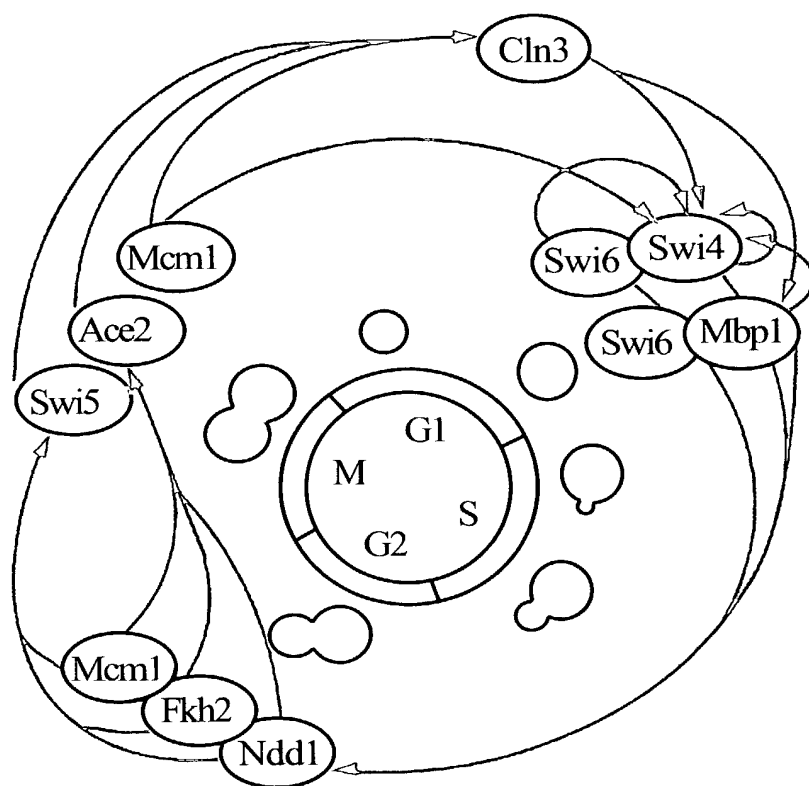


FIGURE 11B



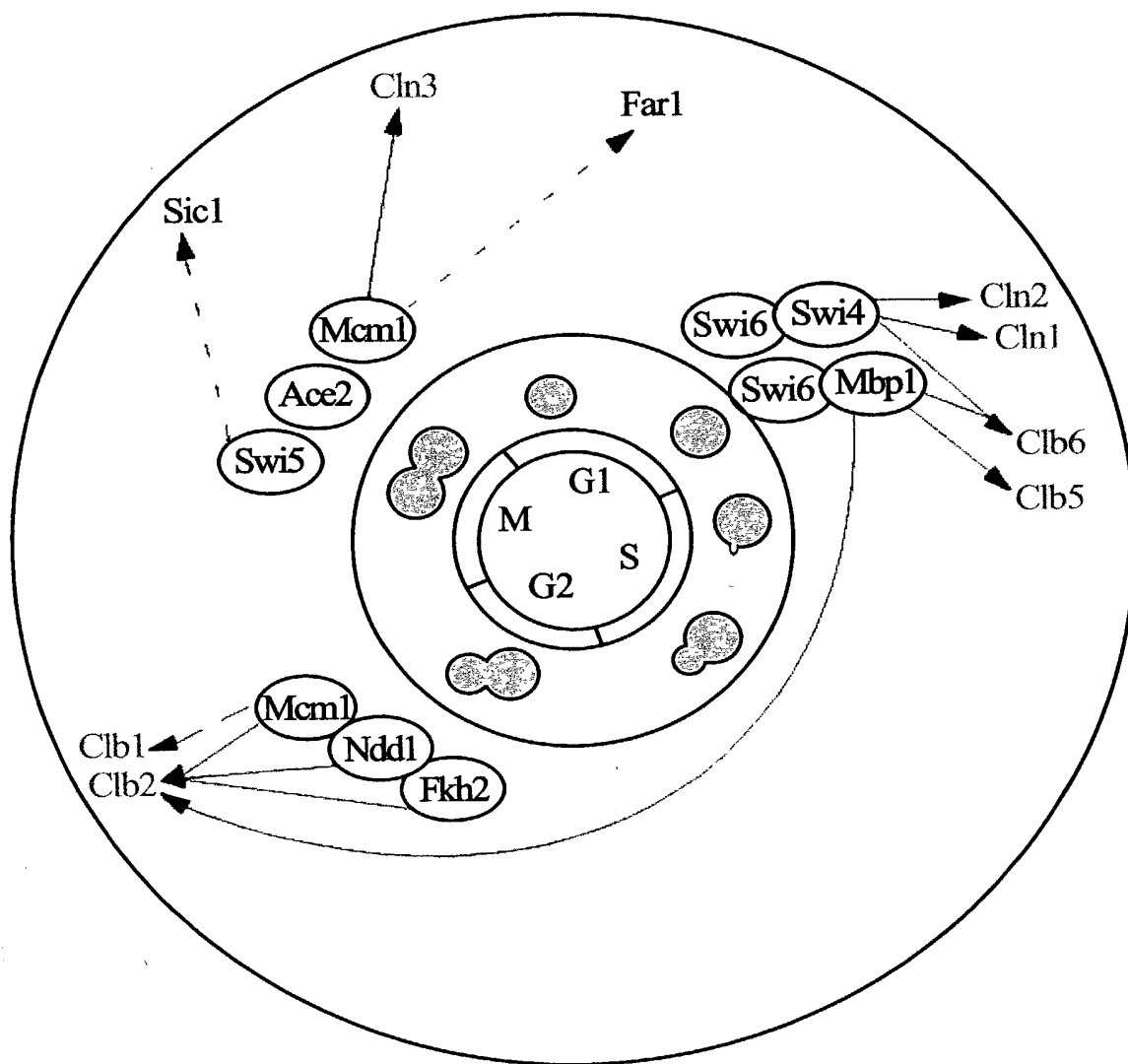


FIGURE 12A



App No.: 10/032,281

311132281.060602

Title: Genome-Wide Location and Function...

Inventors: John Wyrick, *et al.*

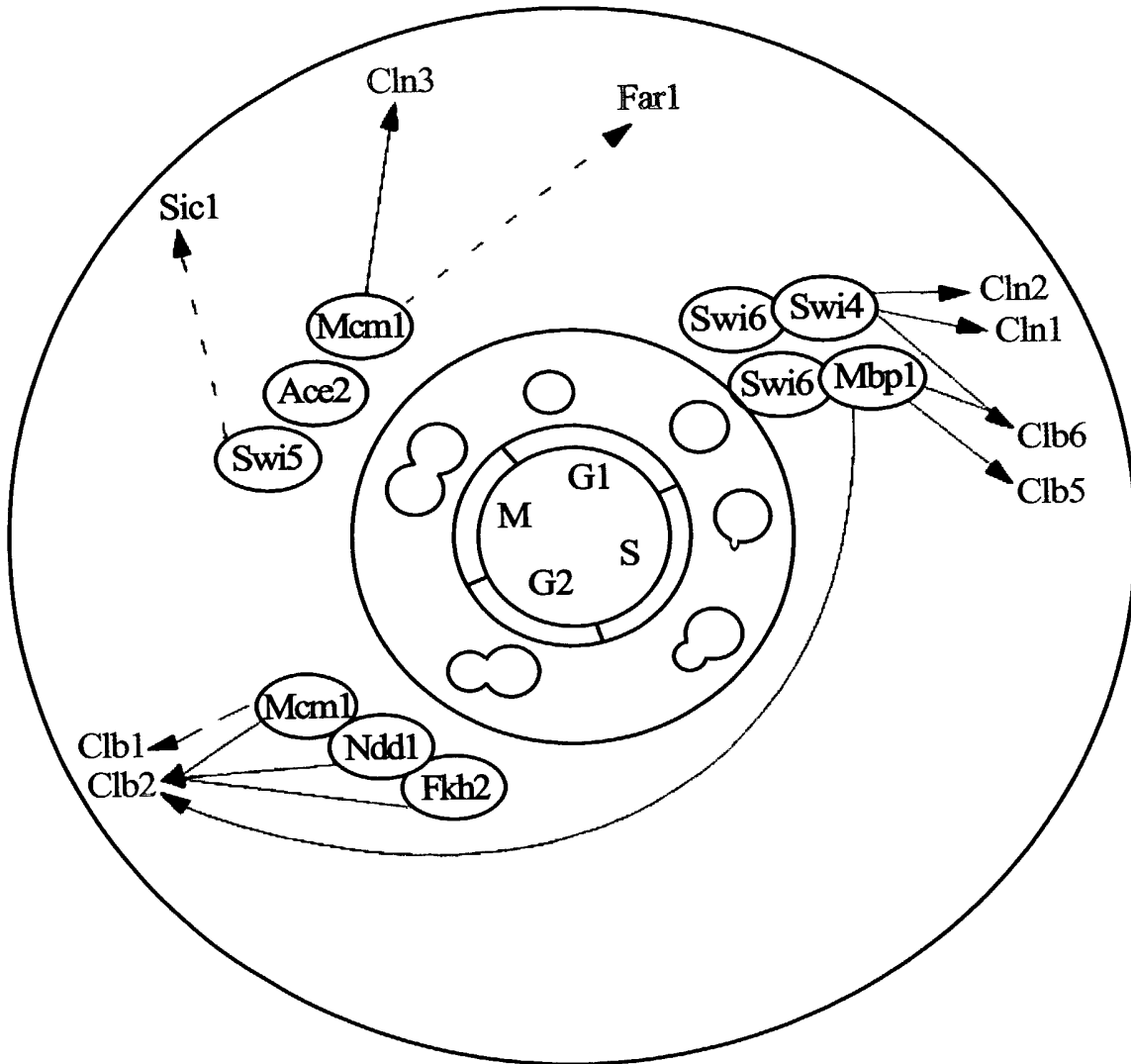


FIGURE 12A



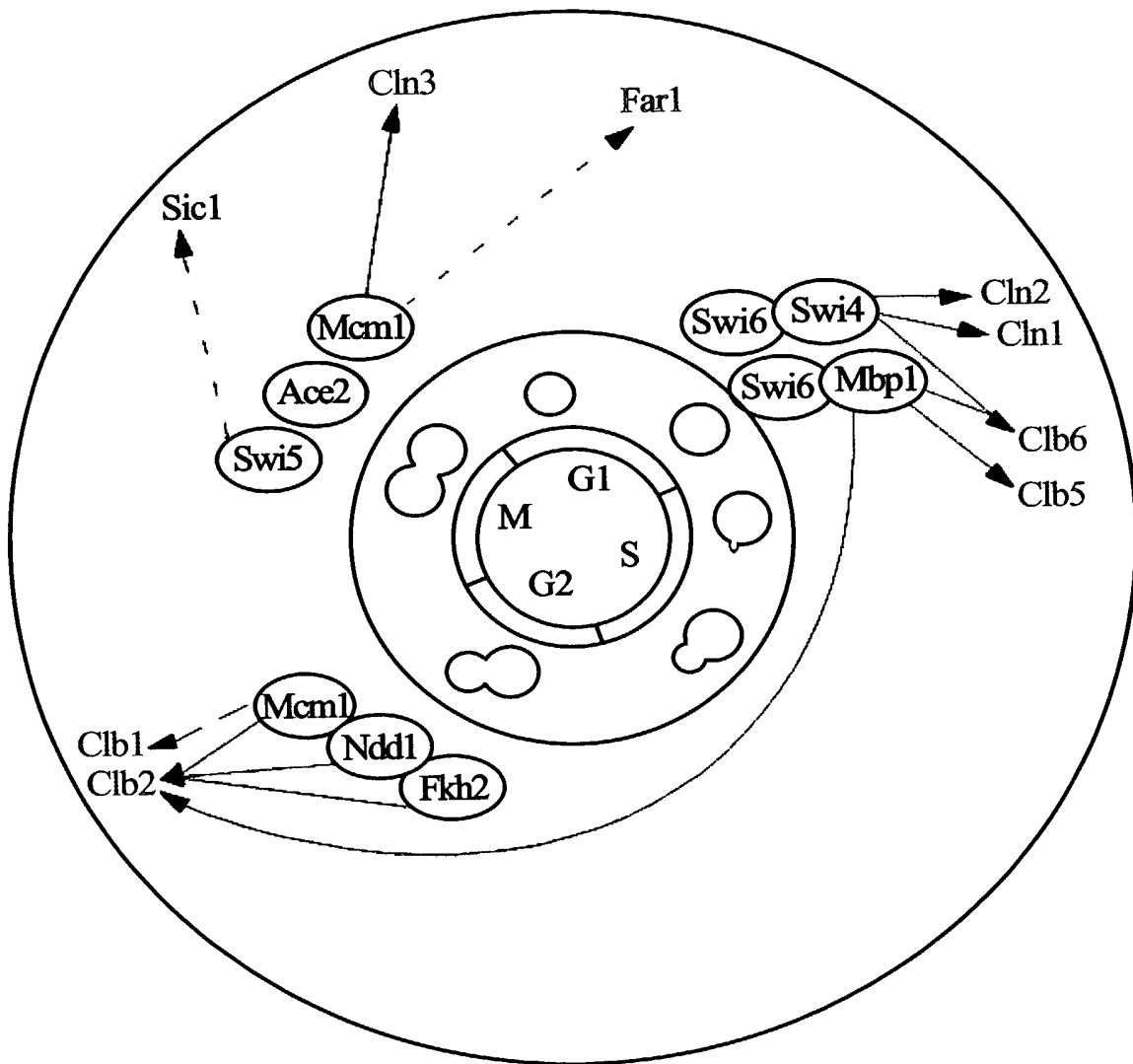


FIGURE 12A



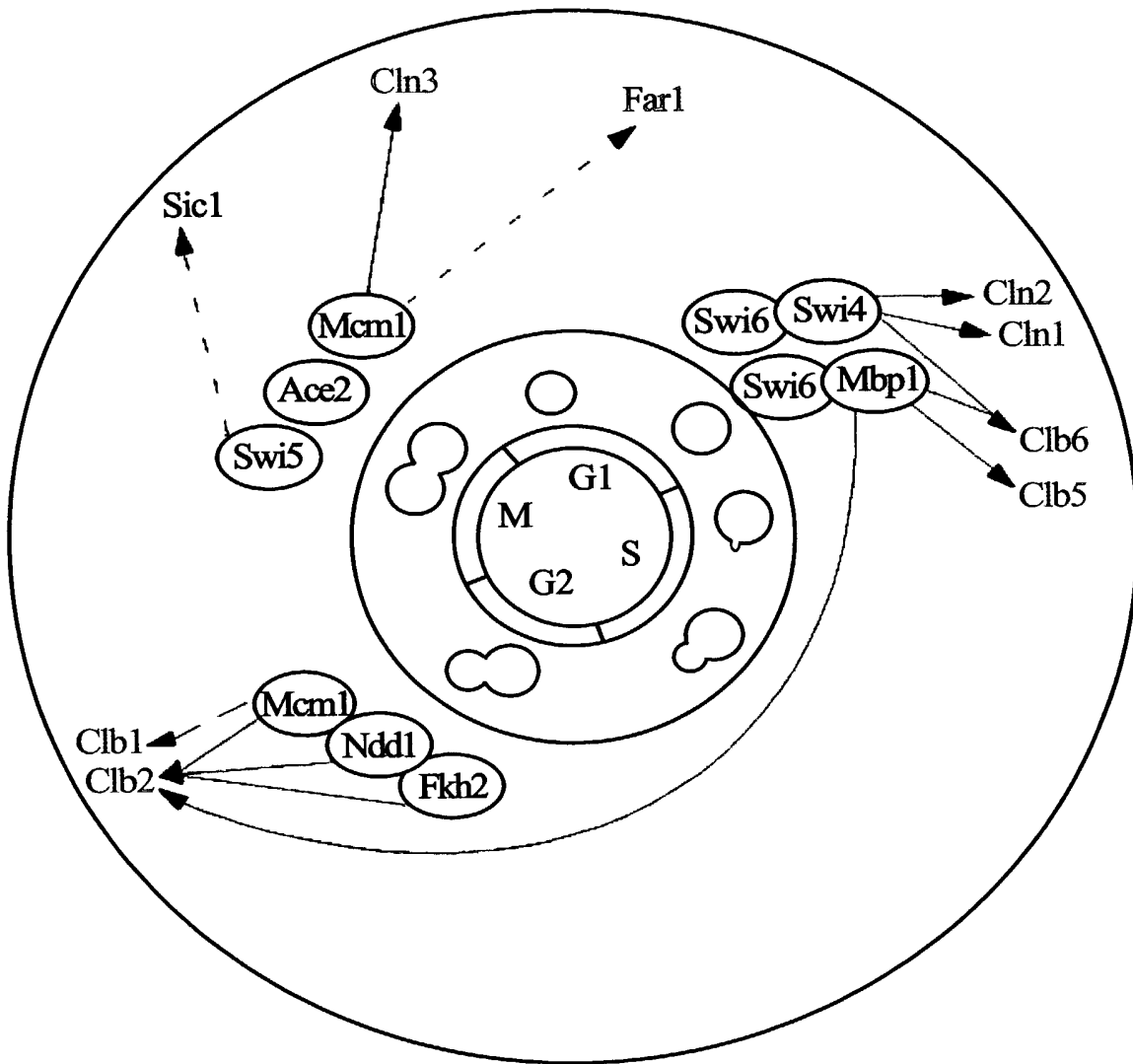


FIGURE 12A



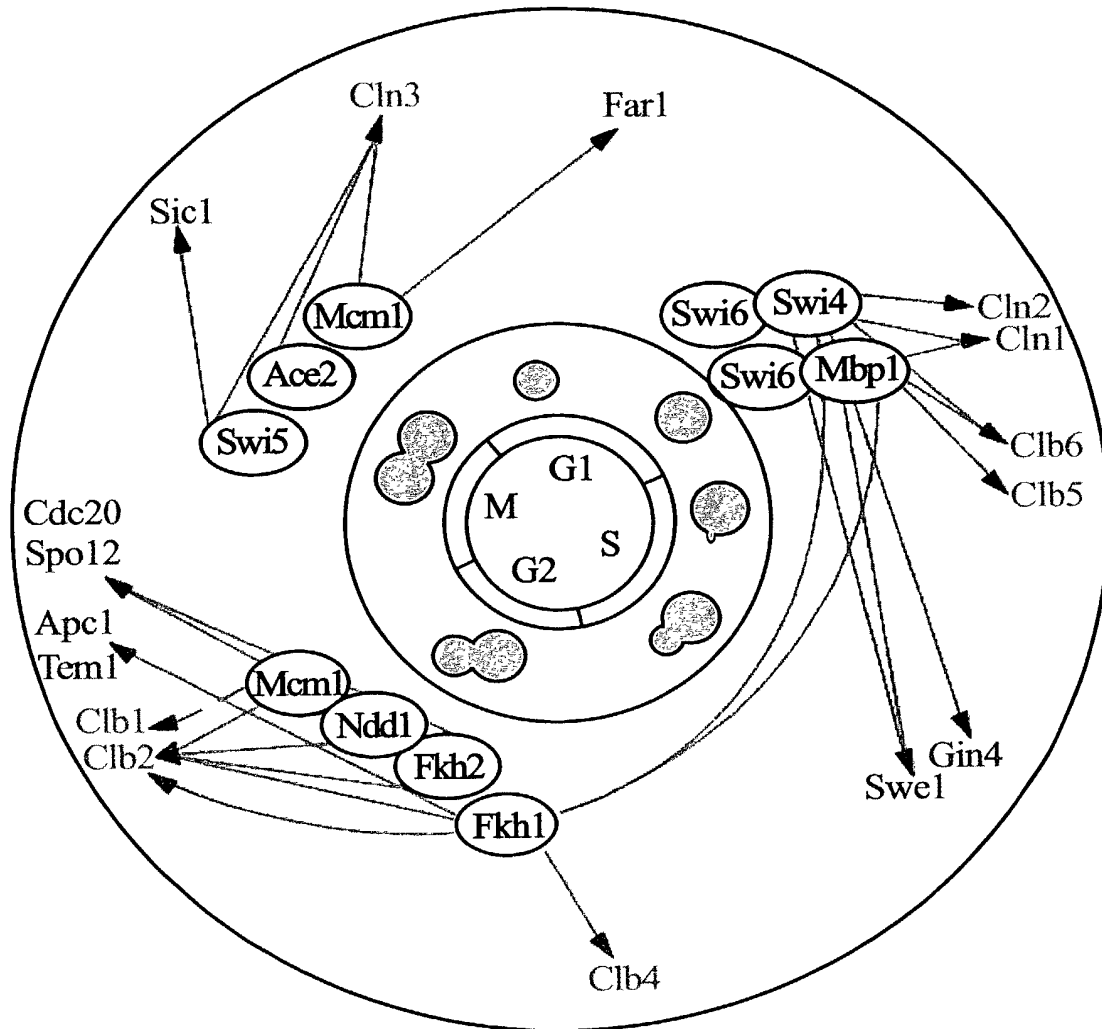


FIGURE 12B



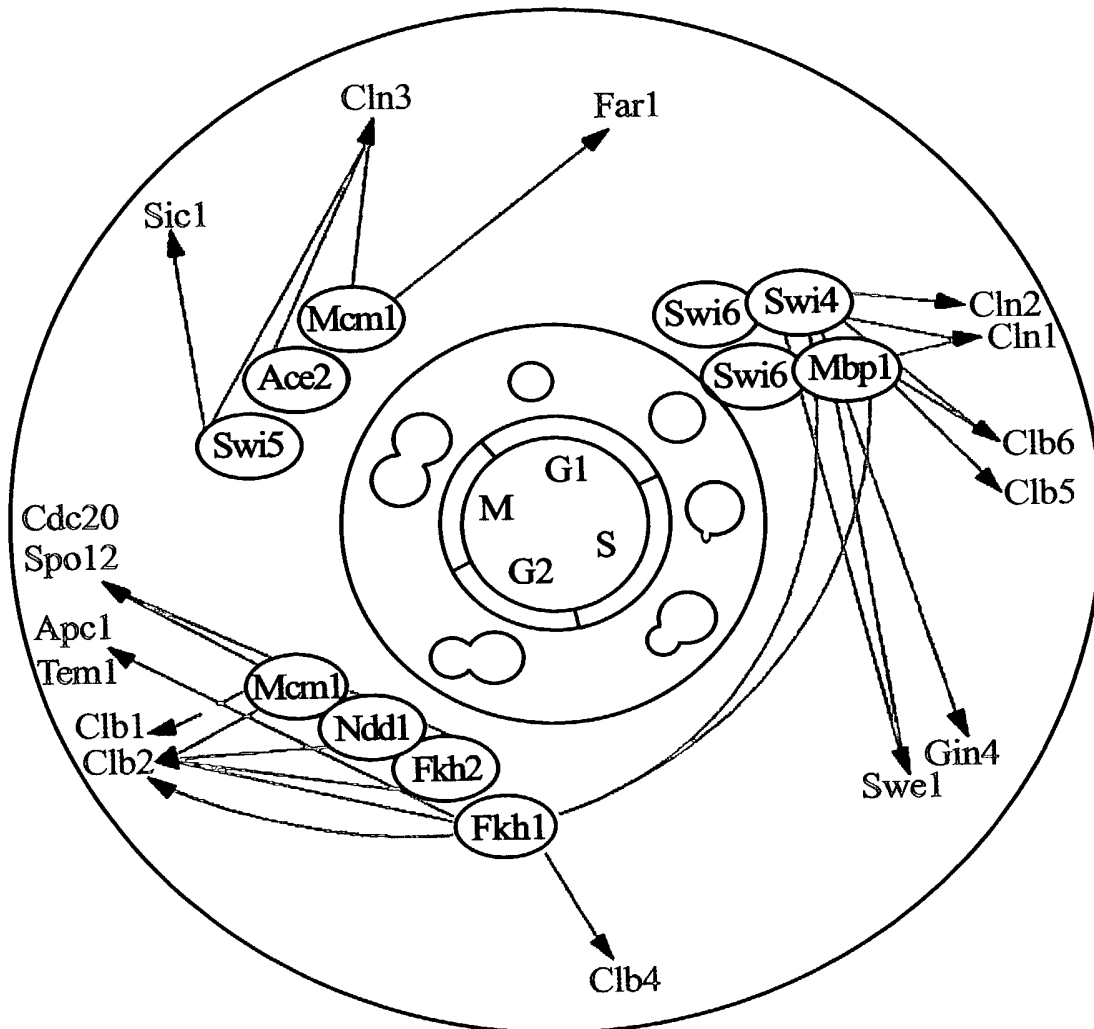


FIGURE 12B



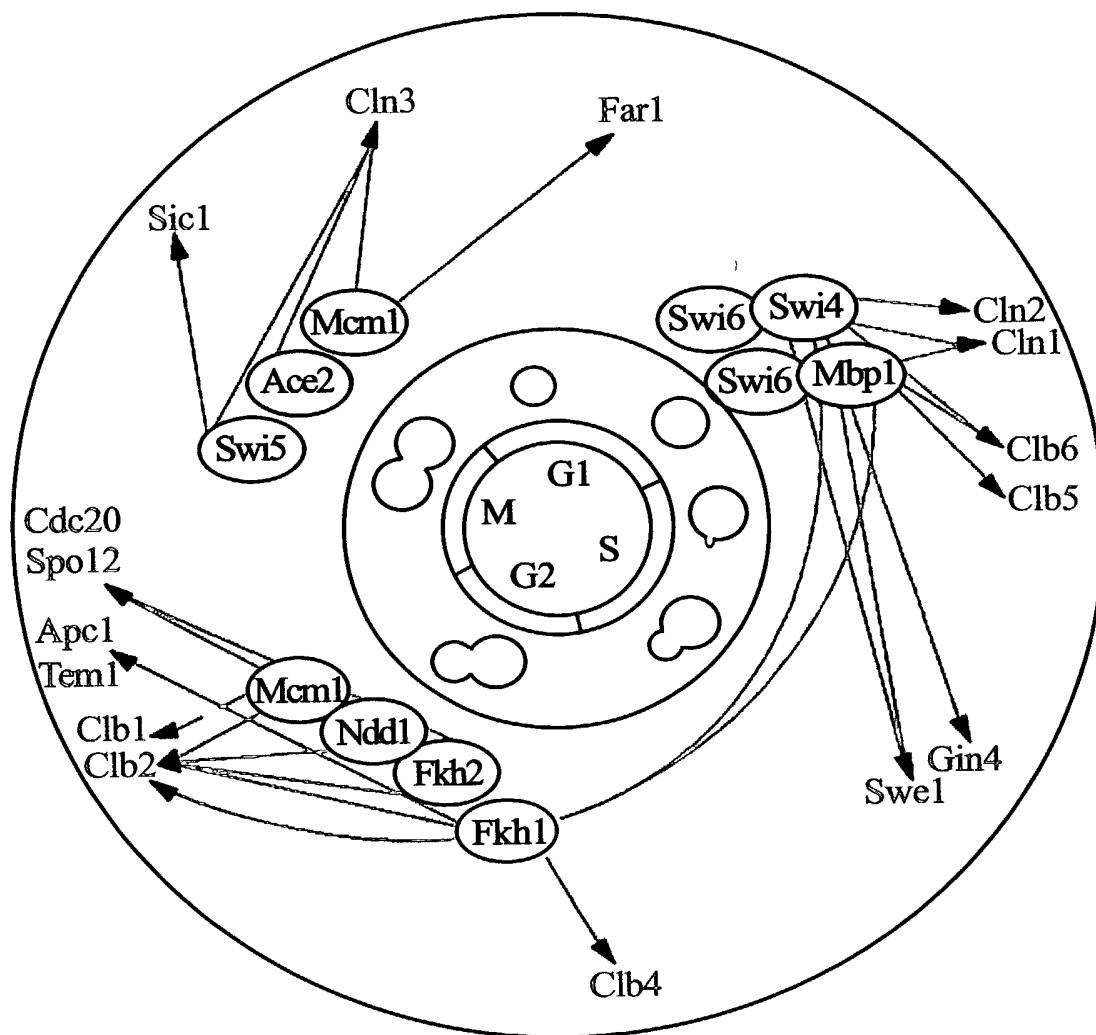


FIGURE 12B



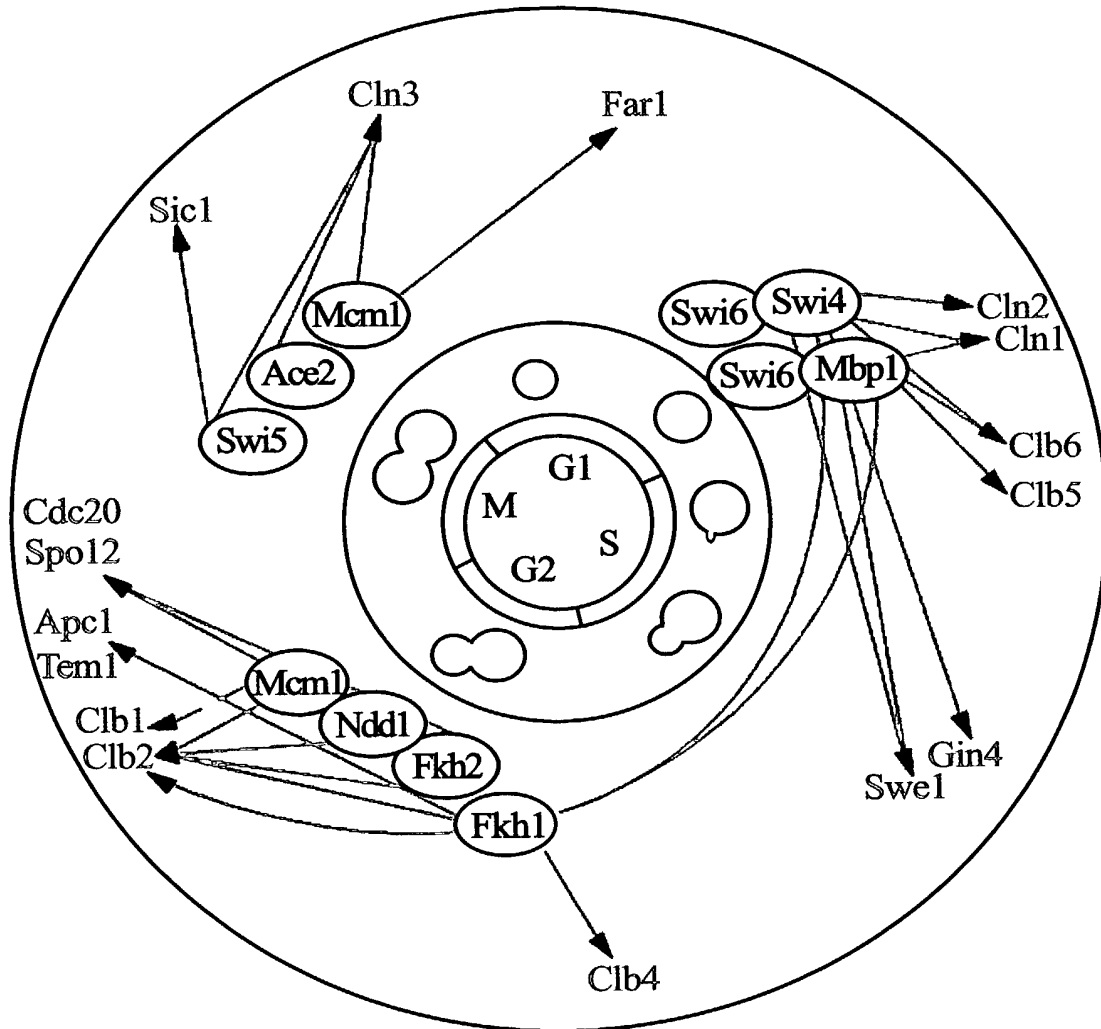


FIGURE 12B



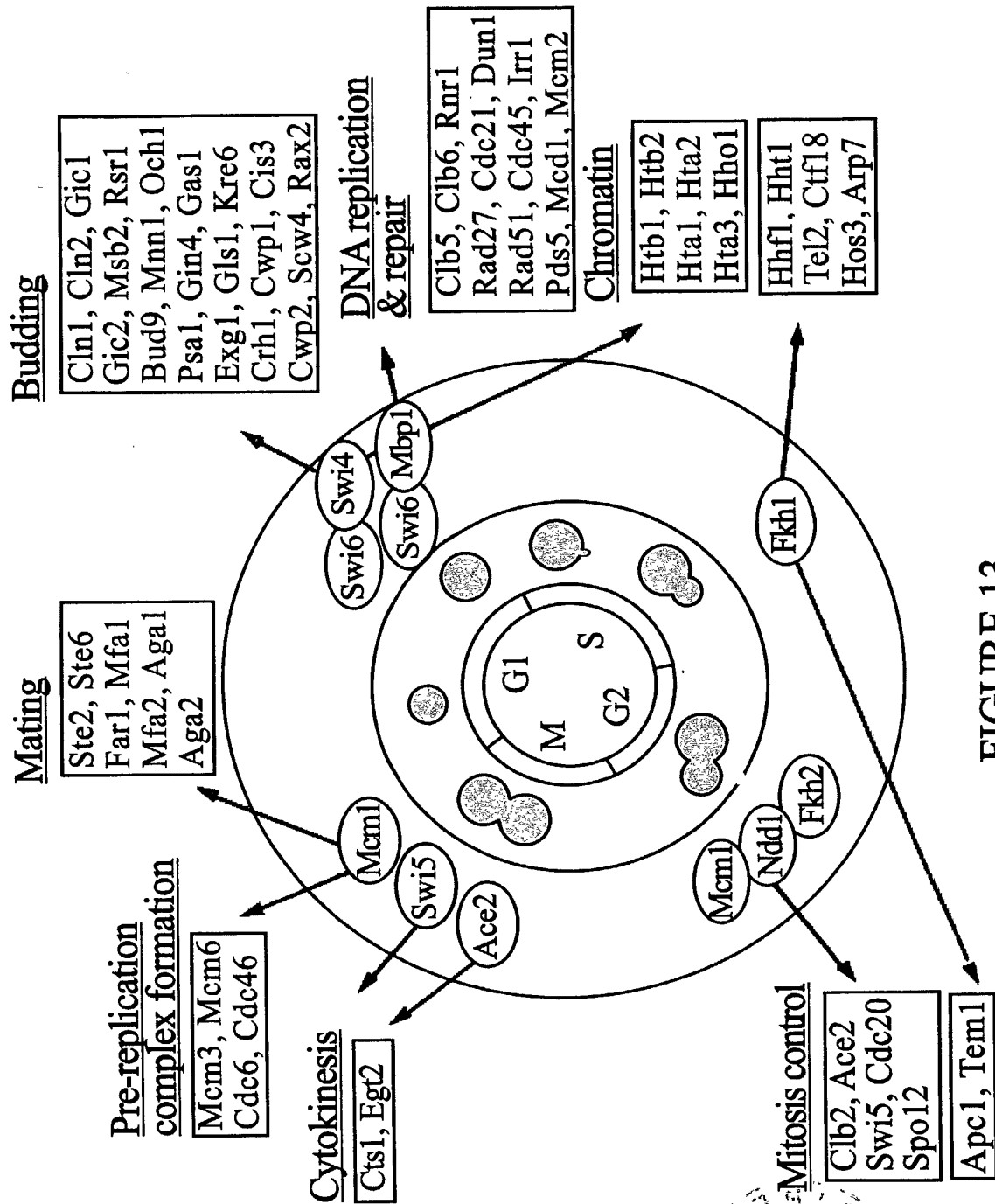
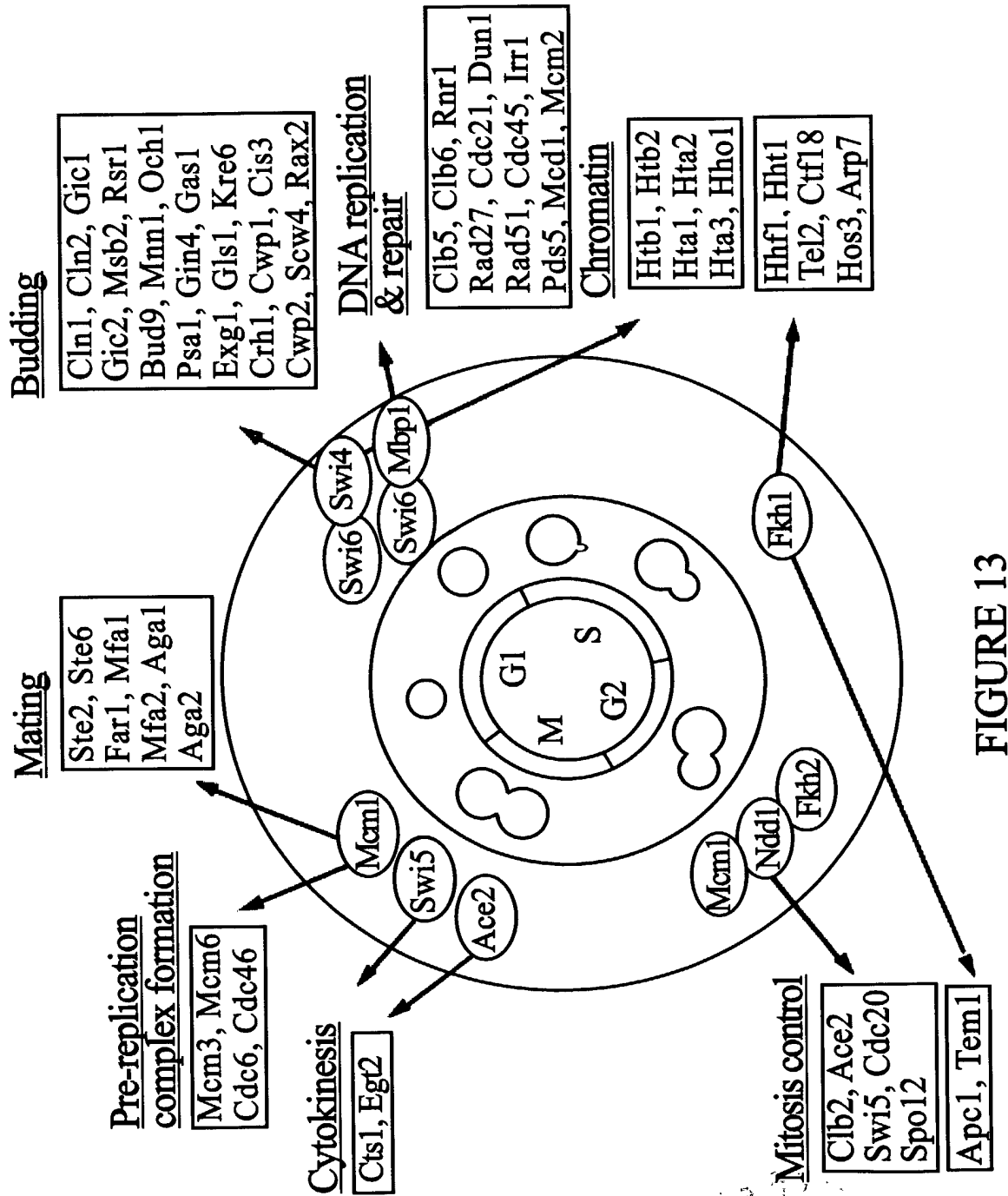
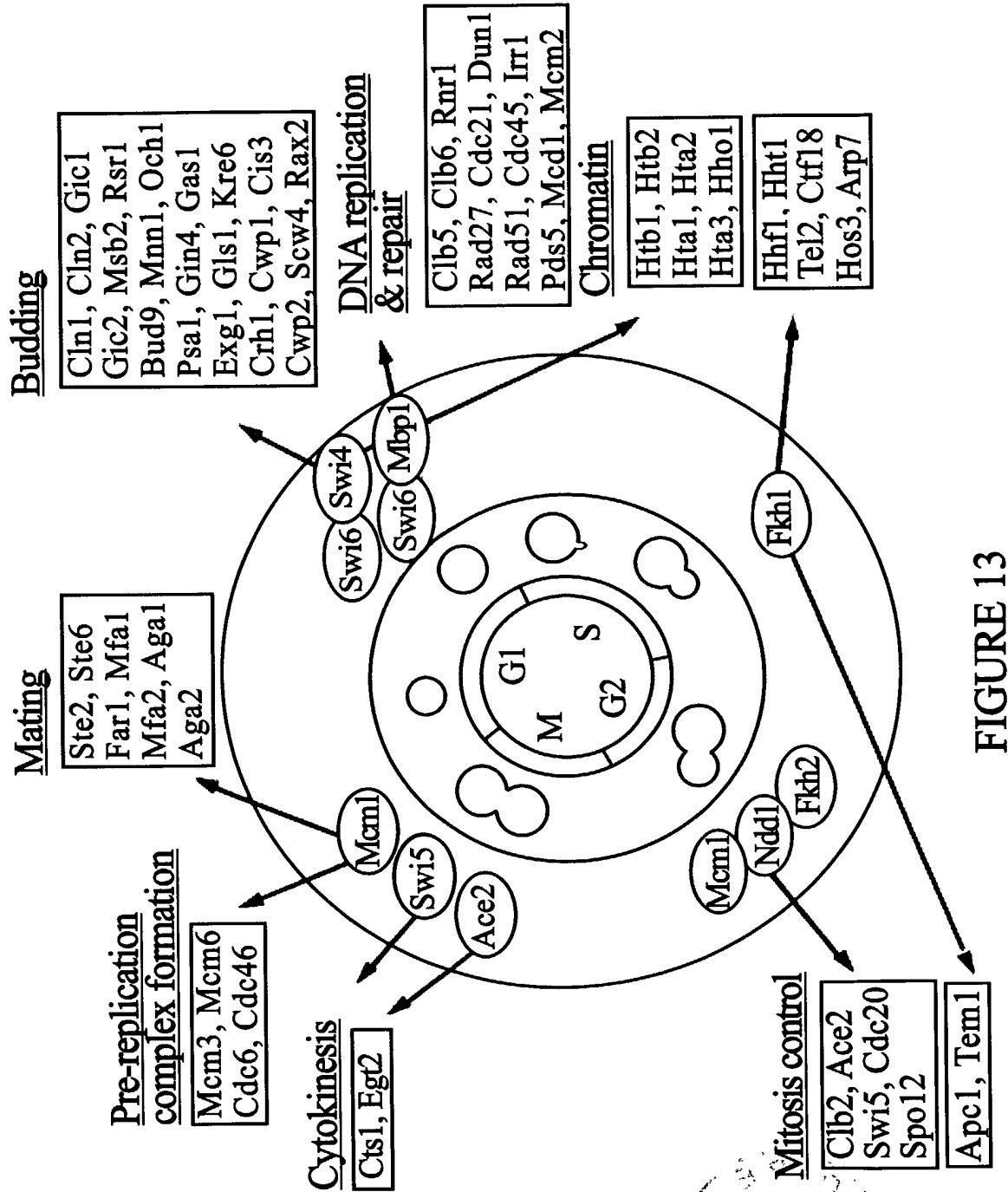


FIGURE 13





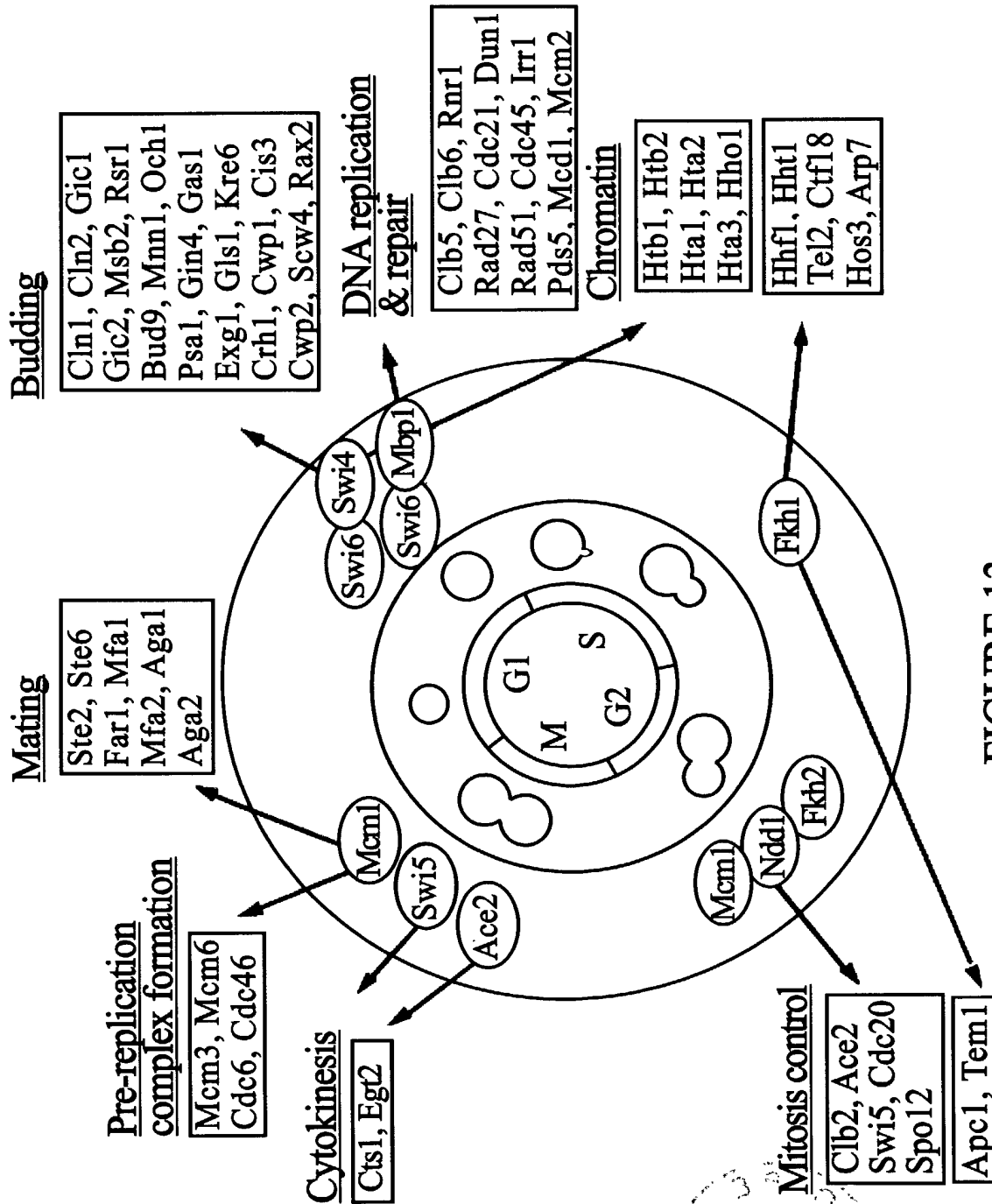


FIGURE 13

Figure 14A

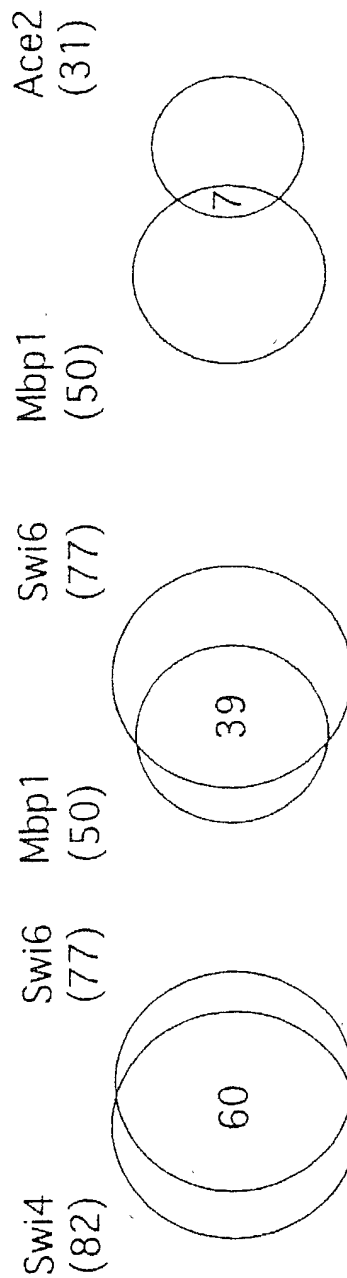
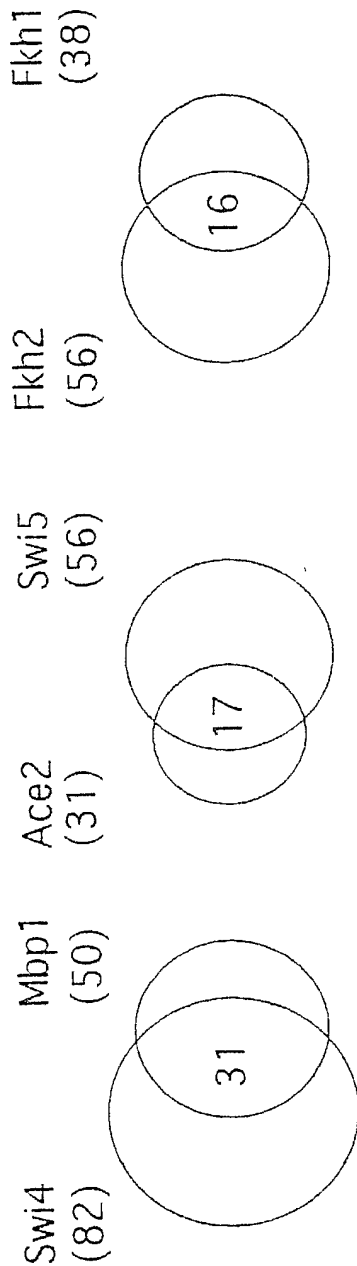


Figure 14C

Figure 14B

